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Medicine, Maidashi, Fukuoka 812-82, Japan
Sequence update by submitter
On Sep 13, 1999 this sequence version replaced
Location/Qualifiers
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Medicine, Maidashi, Fukuoka 812-82, Japan
Sequence update by submitter
3 (bases 1 to 1708)
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Submitted (07-DEC-1996) Biochemistry, Kyun
Grand Pukuoka 812-82, Japan
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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LCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQC
STNESEKPSILVEKCISPEGOPESAVTELQCIWHLLSYMKCSWLDGRWYSPDTNYTL
YYWHRSLEKHQCENIFREGQYFGCSFDLTKVDSSFGOHSVQIMVKDNAGKIKPSFN
IVPLTSRVKDDPPHIKNLSFHNDDLYVQWENPONFISRCLFYEVEVNNSQTETHNVFY
VQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM
SIGKKKNNSTLYITMLLIVPVIVAGAIIVLLLLYLKRLKIIFPPIPDPGKIFKEMFGDQ
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="AAD00510.3"
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쿠 &	GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCACCTAGC 3	
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· Qy	11 GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAAGGCTCAAG 11	
ръ	094 GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAAGGCTCAAG 115	
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Mammalian Gene Collection Program Team
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Akhter, N., Ayele, K., Beckström-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. McDowell, J., Pearson, R., Stantrippe, S., Thomas, P.J., Touchman, J. Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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Homo sapiens interleukin 13 receptor, a
MGC:15228 IMAGE:4300487), complete cds.
BCO009460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 9, 2003 this sequence version replaced gi:14602931.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Director MGC Project.

Direct Submission

Submisted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Proc. Natl. Acad. Sci. U.S.A. !
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Touchman, J.W.,
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gh the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
s: IRAL Plate: 26 Row: n Column: 1.
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/codon_start=1
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/product="interleukin 13 r
/protein_id="AAH09960.1"
/db_xref="geneID:3597"
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/db_xref="GeneID:3597"
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/tlssue="panoreas, epithelioid
/clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"
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Hominidae; Homo
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; sutelec
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                              Homo sapiens
                                                                                                                  alpha 1 chain;
                                                                                                                                                           H.sapiens mRNA for Y09328
                                                                                                 Homo sapiens (human)
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Cloning of the human IL-13R alphal chain and reconstitution the IL4R alpha of a functional IL-4/IL-13 receptor complex FEBS Lett. 401 (2-3), 163-166 (1997)
9013879
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                     GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAGTGAGAAGCCTAGC 390
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Best Local Similarity
Matches 1348; Conserv
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II-13 RECEPTOR.
AL Patent: WO 9720926-A
SANOFI SA (FR)
Other publication AU 7576096 1997
Other publication FR 2742156 1997
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="unassigned DNA"
/db xref="taxon:32644"
/cell_line="LULAIRE: CAKI-1"
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CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA
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                                                                                                                                                        CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
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                                                                                                         GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAG
                                                                                                                                                                                             ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC
                                                                                                                                                                                                             ATAAGAGTCAAAAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1050
                                                                                                                                                                                                                                                                                                              CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCCAGAATTTGAGAGAAATĠTG
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Similarity 99.6%;
48; Conservative
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                                  CATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
                                                                                            AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
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                                                                                 AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
                                                                                                                            GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA
                                                                                                                                                                                                                        ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCAT
                                                                                                                                                                                                                                                                    TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTTGGC
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Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeu
                                                                                                                                                                                                                                                                     Hominidae;
            : WO 0194629-A 6046 13-DEC-2001;
Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                     Homo
                                                                                   Score 1333.8;
Pred. No. 0;
0; Mismatches
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Query Match 96.4%; Score 1333.8; DB 2; Length 4039; Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1; Oy 34 CGGCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGGGCTCTGCGGGCTGTGG 93	/organ.sm="Homo saplens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="EMBL/GenBank Accession No. Y10659" ORIGIN	õ	REFERENCE 1 AUTHORS Alvares, C., Hoxne, D., Peres-da-Silva, S. and Vockley, J.G. TITLE Gene expression profiles in liver cancer JOURNAL Patent: WO 0229103-A 3859 11-APR-2002:	NISM Homo sapiens Eukaryota; Me Mammalia; Eut Hominidae: Ho	917		t. :	GAAACCGACTCTGTAGTGCTGATAGAAAACCTG	1201 CADAA COCACOTOTA CONCENTRADA A A COTOCA SON A COTOCA A CONCENTRADO CADA CONCENTRADO CADA CONCENTRADO CADA COMBINA CONCENTRADO CADA COMBINA CONCENTRADO CADA COMBINA CONCENTRADA CONCE	1231 OCCANTESTECCTCCARTCCTGATCCTGCAAGATTTTTAAAGAAATGTTTGGAGAC 121	1097 GTTCCAGTCGTCGAATCGTCGATCGTGGAATCATTTTTTAATTAA	1111 GTTCCAGTCATCGTGGCAGGTGCABATCATACTACTTTTTTTTTT	977 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 103	917 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACACTCTAGAGC 1	Db 857 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTG 916 Qy 931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACACAGTCAGA 990	Db 797 AATTTTATTAGCAGATGCCTATTTTATGAAGTGAGAAGTCAATAACAGCCAAACTGAGACA 856 Qy 871 ÇATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG 930
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CAAGAAATGAGTATAGGTAAGAAAGCGCAATTCCACCACTCTACATAAACCATGTTACTCACTTACATAAAAAGGGTAAGAATCCAATAGCTCTACATAAAAAAGGGTCAAGATCATAGCTACATTACCTAAAAAAGGGTCAAGGTTCATAGATAACTCCTGCTTTACCTAAAAAAGGCTCAAGGTTCCAAGGTTCCAAGTTCCTAGCTCAAAAAAGGCTCAAGGTTCCAAGTTCCTAGTACTCCTAAAAAAGGCTCAAGGTTCCAAGATTTTTAAAGAAATGTTTGGAGACTIIIIIIIIII	991 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1050	931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGA 990 	871 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTG 930 	811 AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA 870 	751 CATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAAATGGGAGAATCCACAG 810 	691 AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA 750 	631 GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA 690 	571 CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGCTTTGATCTGACCAAA 630	511 ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCAT 570	451 CTTCAATGCATTTGGCACCACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAA	391 ATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAA 450 	331 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGC 390	271 GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAAT 330	211 TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTGGC 270	151 CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA 210	

VQ	Query Ma Best Lo	ORIGIN			CDS	gene		FEATURES source	AUTHORS TITLE JOURNAL	TITLE JOURNAL REFERENCE	REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 10 HSIL13RA LOCUS DEFINITION	₽ 	Db 4	Db Db	Qy Db
34 CGGCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGC	atch 96.4%; Score 1333.8; DB 5; Length 4039; cal Similarity 99.6%; Pred. No. 0; 1348: Conservative 0: Migmatches 2: Indale 3:	VQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLMSNWSQEM SIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKELKIIIFPPIPDPGKIFKEMFGDQ NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"	LCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQC STNESEKESILVEKCISPEGDPESAVTELQCIWHMLSYMKCSWLPGRNTSPDTNYTL YYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVANGKIKPSFN IVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPONTISRCI-PYEVEVNNSCTETHNVPV	/db_xref="GI:1806036" /db_xref="GOA:P78552" /db_xref="UniProtKB/Swiss-Prot:P78552" /translation="MEWPARLCGLWALLL.CAGGGGGGGGGAAPTETOPPVTNI.SVSVRN	441327 /gene="TL-13RA" /codon_start=1 /protein_id="CAR71669.1"		/olyanism="nome sapiens" /mol type="nRNAM," /db_xref="taxon:9606" /clone="3.1" /cell type="B cell"	Aulx, Plan-Les-Ouates, CH1228, SWITZERLAND Location/Qualifiers 14039					Y10659 Y10659.1 IL13Ra.gen	4	1337 TTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1369	277 GAAACCGACTCTGTAGTGCTGATAGAAAACCTG		1157 ATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC 1216 1231 CAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG 1290
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1111 GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAAGGCTCAAG 1170	1051 CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT 1110 	991 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1050 	931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGA 990 	871 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAATTTGAGAGAAATGTG 930 	811 AATTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA 870 	751 CATATTAAAACCTCTCCTTCCACAAIGATGACCTATATGTGCAATGGGAGAATCCACAG 810	691 AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA 750	631 GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA 690	571 CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTGTTTGATCTGACCAAA 630 	511 ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCAT 570	451 CTTCAATGCATTTGGCACAACCTGÀGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAAT 510	391 ATTTTGGTTGAAAAAIGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAA 450 	331 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAGTGAGAGCCTAGC 390	271 GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAAT 330 	211 TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTTGGC 270	151 CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGGACAGTAATATGGACA 210 	94 GCGCTGCTGCTGCGCCGGCGGGGGGGGGGGGGGGGGCGCGCCTACGGAAACT 150	17 CGCCGGGCTCCGAGGCGAGGGCTGCATGGAGTGGCCGGCGCGCGC

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Klausner, R.D., Collins, F.S., Wagner, L., Sheamen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bonaldo, M.F., Casavant, T.L.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
P. 12477932
                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 34 Row: k Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Peatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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                                                                                                                  organism="Homo sapiens"
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/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
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                          AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
                                                                                                                               GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA
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/protein_id="AAH15768.1"
/db_xref="GI:16041775"
/db_xref="GeneID:3597"
/db_xref="MIM:300119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MECPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVEN
LCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQC
STNESEKPSILVEKCISPEGOPESAVTELQCIWHNLSYMKCSWLPGRRYSPDTNYTL
YYWHRSLEKIHQCENIFEGQYFGCSFDLTKVGUSFEQHSVQIMVKDNAGKIKPSTN
YWHRSLEKIHQCENIFEGQYFGCSFDLTKVGUSFEQHSVQIMVKDNAGKIKPSTN
IVPLTSRVKDDPPHIKNLSPHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFY
VQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKIMSNWSQEM
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/db_xref="GeneID:3597"
/db_xref="MIM:300119"
4R_____1331
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1 (bases 1 to 1572)
Aman, M.J., Tayebi, N.,
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J. Biol. Chem. 271 (46),
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 /organism="Homo sapiens'
/mol_type="mRNA"
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LCTVIWTWNPEGASSNCSLWFFSHFGDY
STNESEKFSILVEKCISPEDEDPESAVIELOCIUHNLSYNKCSWLPGRNTSPDTNTL
YYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSFEQHSVQIMVKDNAGKIKPSFN
1 VPLTSRVKPDPPHIKNLSCHVPGULPDTLIVVRIVKTNKLCYEDDKNSQTETHAVDFY
VQEAKCENPEEERNVENISCHVPGULPDTLIVVRIVKTNKLCYEDDKNSQTETHAVDFY
VQEAKCENPEEERNVENISCHVPGULPDTLIVVRIVKTIVKLCYEDDKNFN
SIGKKENSTLYITMLLIVPVIVADAIIVLLLXLKRLKIIFPPIPDPGKIFKEMFGDQ
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/chromosome="X"
85. .1368
/function="cytokine receptor"
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/product="interleukin-13
/protein_id="AAB37127.1"
/db_xref="GI:1695876"
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99.5%;
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AB209849.1
Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S., Ohara,O., Nagase,T. and F.Kikuno,R.
Direct Submission
Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,
                                                                                                             None
                                                                                                                                                                                                                                                                                         Homo
                                                                                             Published Only in Database
                                                                                                                       Ohara,O., Nagase,T.
                                                                                                                                     Totoki,Y.,
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AGAAGGTGATCCTGAGTCTGCTGTGACTTCAATGCATTTGGCACAACCTGAGCTA
                                                                                GTGTAGCACCAATGAGAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCC
                                                                                                GTGTAGCACCAATGAGAGTGAGAAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCC
                                                                                                                                                   AACTCGTCGTTCAATAGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCA
                                                                                                                                                                                                          TGTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAA
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URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930, Fax:81-438-52-3931)
This work was supported in part by the National Project on Protei Structural and Functional Analysis , Ministry of Education, Cultu , Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan. e-mail: aktanaka@postman.riken.go.jp
URL: http://protein.gsc.riken.go.jp/.
/protein_id="BAD93086.1"
/db_xref="G:6209284"
/translation="EMPALCGUMALLLCAGGGGGGGAAPTETOPPVTNLSVSVENL
/translation="EMPALCGUMALLLCAGGGGGGGGAAPTETOPPVTNLSVSVENL
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TNESEKPSILVEKCISPPEGDFSAVTELQCIIHNLSWKCCSNLPGRNTSPDTNYTLY
YWHRSLEXIHOCENIFEEGQYEGCSFPDLTKVEDSSFEOHSVOLMVKDNAGKIKPSFNI
YWHTSLEXHOCENIFEEGQYEGCSFPDLTKVEDSSFEOHSVOLMVKDNAGGTETHNVFYV
QEAKCEMPEFENVENTSCFMVPGYLPDTLNTVRIRVETYLVELXERLKIIIFPPIPDFGKIFKEMFGDQN
DDTLHWKKYDIYEKQTKEETDSVVLIENLKKASO"
                                                                                                                                                                                                                                                                                                      /product="interleukin
variant"
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="interleukin 13 receptor, alpha 1 precursor variant"
/inference="non-experimental evidence, no additional
details recorded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="aorta endothelial
/note="this clone is also named
vector:pBluescriptII SK plus"
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                                                                                                                                                                                                                                                                                                                                                                     codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                 note="Start codon is
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ef01196"
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CGGGGGCGGGGCCGCCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTC CGGGGGCGGGGG----CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTTGAGTGTCTC Conservative 94.3%; 0, Score 1304.8; Pred. No. 0; 0; Mismatches В 2: 5 Indels Length ω •• Gaps 120 179 60 122 1;

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                                              AY892945 1284 bp mRNA linear synthetic construct Homo sapiens clone FLH141766.01L receptor alpha 1 (IL13RAL) mRNA, partial cds.
                                      AY892945
 synthetic construct
             Human ORF project.
                         AY892945.1 GI:60654342
                                                                                                                                                              AAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTCTTCCTGATACTTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTA 1019
                                                                                                                                        AAGA
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JOURNAL
                                                                                                                                                                                                   Matches 1277;
                                                                                                                                                                                                               Query Match
Best Local
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Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sweences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (05-JAN-2005) Biological
Submitted (05-JAN-2005) Biological
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1 (bases 1 to 1284)

Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphae,Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Williamson,J. and LaBaer,J.

Cloning of human full-length CDS in Creator (TM)
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Pred. No. 0;
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Zuo,D., Tayc
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Zuo,D., Taycher,E.,
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537 480	78 TACATGAAGTGTTCTTGGCTCCCTGGAAGGA 	
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417 360	58 CAGTGTAGCACCAATGAGAGTGAGA 	
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Search completed: July 8, 2006, 00:13:42 Job time: 8122 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

18 1333.8 96.4 4039 11 ABD20879	17 1333.8 96.4 4039 10 ABZ97030	16 1333.8 96.4 4039 6 ABN97361	.8 96.4	.8 96.4	œ	.8 96.4	.8 96.4 4038	.8 96.4	96.4	.8 96.4	96.4		.8 96.4	.8 96.4	3 1333.8 96.4 3999 3 AAF21335	2 1333.8 96.4 3999 3 AAA35213	. 1 1383 100.0 1383 2 AAT66165	No. Score Match Length DB ID	Result Query	æ	SUMMARIES
Abd20879 Human pul	Abz97030 Human nuc	Abn97361 Gene #385	Abk84753 Human cDN	Abl67709 Oesophagu	Aaf21336 Human low	Aaa35214 Human ade	Adn62574 Human cDN	Adl71811 Human int	Aaa88907 Human int	Aat85827 Human int	Aec15897 Human int	Human	Abd20878 Human pul	Abz97029 Human nuc	Aaf21335 Human low	Aaa35213 Human ade	Aat66165 Human int	Description			

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AAS59956 AAA09049 AAD63743 AAD22979	AAS59954 AAA09050 AAD63744 AAS59957	ABK35719 ADO26893 AAS59955	ADF17834 ABK35718 AAF98394	AAF21338 ABZ97032 ABD20881 ADV42774	ACN41073 ADX97460 ADB47358 ADB477356 AAX77356 AAA90388	ADL82842 ADN04503 ADR24772
Aas59956 Canine in Aaa09049 IL-13/IL- Aad63743 Human IL- Aad22979 Human sol	44	cDNA se 3 cDNA e Canine	40.4	Adv42774 Human psy	m o u	

ALIGNMENTS

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RESULT 1
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AAT641A
AAT64
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22-DEC-1995;
09-SEP-1996;
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DNA encoding animal haemopoietin receptor which interacts with

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Best Local Sim
Matches 1383;
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by IgE production.
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TTAACTTCCCGTGTGAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGAT
                                               GTCCAAATAATGGTCAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCT
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   03-AUG-1999;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                        and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from bulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration;
                                                                   Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;
                                                                                                                                     pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification c
                                                                                                                                                                                                                                                                                                                                                  transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction
                                                                                                                                                                                                                                                                                                                                                                                                                                            chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes low adenosine
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                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 1336-1337; 1592pp; English.
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  96.4%;
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Score 1333.8; DB 3; Length 3999; Pred. No. 0;
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Transcon Co

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The invention relates to a novel pharmaceutical composition, which has first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3 intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammatory; antione; immunosuppressive; cytostatic; gene therapy antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
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Best Local Similarity
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RESULT 5
ABD20878
ID ABD2
XX ABD2
XX ABD2
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX FR
KW resp
KW surf
KW pulm
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PF 23-A
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                                                                                                                                                                                                                                                                                                                                 Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
                                                                                                                                                                 23-APR-2002; 2002WO-US013143
                                                                                                                                                                                                                                                                      Homo
                                                                                                                                   24-APR-2001; 2001US-0286036P
                                                                                                                                                                                                                                                                                                     pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pulmonary
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                                              Li Y,
Tang
                                                                                                                                                                                                                                                                                                                     chronic obstructive pulmonary disease;
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                                                                 Sandrasagra A,
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cancer; bronchitis;
                                                                Aguilar
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CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a CC beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered CC composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to CC reduce the amount of target polypeptide present in the lungs. The CC pulmonary obstruction, and/or bronchoconstriction and/or lung CC inflammation, allergies and/or surfactant hypoproduction are associated CC with a disease or condition such as pulmonary vasoconstriction, cC inflammation, allergies, asthma, impeded respiration, respiratory CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. CC The reduced adenosine content of the anti-sense oligos corresponding to Cthymidines present in the target RNA serves to prevent the breakdown of CC thymidines present in the target RNA serves to prevent the breakdown of CC thymidines present in the target RNA serves to prevent the breakdown of CC prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The compo of the invention has antiallergic, antiinflammatory, antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies a reducing adenosine sensitivity, levels of adenosine (A) or (A) is surfactant depletion or hyposecretion, when administered to a majority of the surfactant of a surfactant control or hyposecretion, when administered to a majority of the surfactant depletion or hyposecretion, when administered to a majority of the surface of the surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted nucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a novel composition
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3999 BP; 1127 A; 826 ς; 882 G; 1164 T; 0 U; 0 Other;

Query Match Best Local (

Similarity

96.4%;

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RESULT 6
ACF87407
ACF87407
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AC ACF8
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DE Huma
Human SIRS/sepsis diagnostic marker DNA fragment
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02-APR-2003; 2003DE-01015031
08-AUG-2003; 2003DE-01036511
02-SEP-2003; 2003DE-01040395
                                                                                                                   31-MAR-2004;
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                                                                                                                                                                             WO2004087949-A2
                                                                                                                                                                                                                                      Systemic inflammatory response syndrome; SIRS; antibacterial; immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
                                (SIRS-) SIRS
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                              LAB GMBH
   Reinhart
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   ᄌ
   Saluz
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   Straube
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 Zipfel
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Deigner
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In vitro detection of systemic inflammatory conditions, for e.g. monitoring progression, expression of disease-related genes. response syndrome and related, comprises detecting abnormal

Disclosure; Page; 75pp; German.

The invention relates to a novel method for in vitro detection of CC systemic inflammatory response syndrome (SIRS). The method comprises CC detecting abnormal expression of disease-related genes, or their CC associated peptides. The method of the invention demonstrates and the interpretation immunosuppressive and antiinflammatory applications and CC may be used for early differential diagnosis, monitoring progression, CC assessing risk, assessing the likely response to treatment and for post CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and CC sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating CC useful as calibrants in assays for the specified diseases, for evaluating activity or toxicity in screening for active agents and/or for CC preparation of agents for treatment or prevention of the specified CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic CC marker DNA fragment of the invention. Note: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at the will be published CC disclosed within the specification, however, these have not been taken into the proposition of the sequence of a proposition and the proposition of the sequence of a proposition of a proposition of the sequence of a proposition of into account during indexing due to inconsistencies in application

Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Conservative

<u>.</u>

96.4%;

Score 1333.8; Pred. No. 0; 0; Mismatches

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14 - ARR - 2004
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18 - FEB - 2004
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RNA interference; gene silencing; cancer; hyperproliferation; neoplasm; cytostatic; viral infection; infection; virucide; inflammation; antiinflammatory; autoimmune disease; inflammatory; autoimmune disease; inflammatory pulmonary disease; respiratory disease; respiratory-gen.; pulmonary disease; respiratory disease; respiratory-gen.; neuroprotective; renal disease; endocrine disease; genitourinary disease; nephrotropic; endocrine-gen.; liver disease; gastrointestinal disease; hepatotropic; ocular disease; ophthalmological; reproductive disorder; infertility; antiinfertility; gynecology and obseterics; andrology; mitochondrial disease; prion disease; degeneration; interleukin-13 receptor alpha 1; IL-13 receptor alpha 1; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin-13 receptor alpha 1 (IL-13RA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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/*tag= a /product= Location/Qualifiers "Interleukin-13 receptor alpha 1 (IL-13RA1)"

2001US-0311865P.
2002US-0358580P.
2002US-0362016P.
2002US-0363124P.
2002US-0386782P.
2002US-0406784P.
2002US-0406784P.
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cc acids (siMAs) which downregulate expression of receptors for interleukin-
cc receptor gamma (IL-2RG)) by RNA interference. The invention also relates
cc to similar siNAs which interfere with the expression of the ligands for
cc these receptors, namely IL-3 and IL-4. The siNAs of the invention; may or
cc may not comprise ribonucleotides, can contain deoxyribonucleotides, can
comprise sense and antisense regions, or alternatively are assembled from
cc the siNAs include short histense regions, or alternatively are assembled from
cc the siNAs include short histense regions, or alternatively are assembled from
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cc the siNAs include short histense regions, or alternatively are assembled from
cc the siNAs include short histense regions, or alternatively are assembled from
cc thistense to pharmaceutical compositions comparising an siNA targeted to
cc the siNAs include short histense regions, or alternatively the siRNAs shown in
cc target genes in cells, tissue explants or organisms (e.g., by ex vivo
cc target therapy), or in grafts and transplants for the treatment of a
curiety of interleukin-related conditions. They may be used in the
curiety of interleukin-related conditions. They may be used in the
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curiety of interleukin-related conditions. They are an altonomial diseases, renal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 32; Page; 127pp;
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GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGC
                                                               GACAAACAAGATAAGAAAATAGCTCCGGAAAACTCGTCGTTCAATAGAAGTACCCCCTGAAT 330
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes human interleukin-13 (IL-13) alpha receptor. The invention relates to new purified peptides comprising 380 or 427 amino acid sequences, which are receptors for interleukin-13 (IL-13); the 380 and 427 aa proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13R while IL-13R alpha has low affinity, but acquires high affinity when associated with the IL-4 receptor. Nucleic acids encoding IL-13R beta and alpha are used as idagnostic probes to identify aberrant synthesis or genetic anomalies of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and callergy. Il-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of IL-13R receptors; when coupled to a toxin also for treatment of of standard overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R
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            The present sequence is that of cDNA encoding a protein (see AAB19907) CC capable of binding human interleukin-13 and/or human interleukin-24 (IL-4) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR or isolated from a database using mouse IL-13 receptor alpha. To isolate the cDNA, PCR coll cDNA. The presence using mouse IL-13 receptor alpha. The primers were used to amplify human IL-13 receptor cDNA from activated tonsilar B cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10 cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10 cell cDNA. The primers cell cDNA insert provided the present sequence. This IL-13 receptor alpha-1 can be used to inhibit IL-13 or IL-4 induced IGE synthesis in B cells, useful in the treatment of diseases where IGE or Th2 differentiation plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, ecdema, asthma or AIDS. Antibodies raised against the polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of them which have been shed contentials, allergies, rhinitis, eczema, asthma, AIDS, lupus
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P-PSDB; AAB19807.
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atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
dermatological; antiasthmatic; antiallergic; therapy; diagnosis;
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GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGA
                           GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGAGTCAGA
                                                                                                                         CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCCAGAATTTGAGAGAAATGTG
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12-NOV-1997; 97US-00969125
06-APR-2000; 2000US-00545002
                Bonnefoy
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                                                                                                                                                                                                              04-MAR-2004
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; asthma; AIDS; gene therapy; gene;
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P-PSDB; ADL71812.
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Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS, comprises administering a polypeptide or soluble polypeptide.

1; SEQ ID NO 8; 27pp; English.

The invention relates to polypeptides capable of binding human interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The invention also relates to a method of treatment of a disease in which III3 and II4 cause adverse effects. The method is useful for treating a disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides of the invention are useful in raising antibodies. It is also useful in gene therapy. The present sequence is human interleukin-13 receptor alpha (IL-13 Ralpha) cDNA.

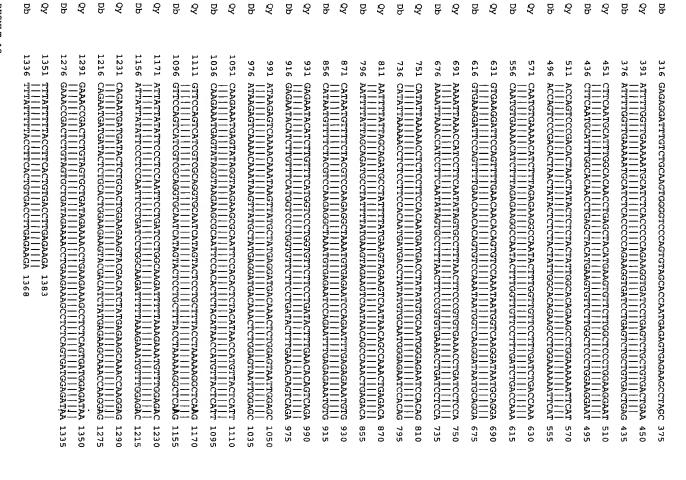
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AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAAACCTGATCCTCCA
                                                                   GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA
                                                                                                                                          CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (ADN62574), CC which encodes the mature form of a polypeptide capable of binding human CI II-13 (interleukin 13) and/or binding human II-4 (designated II-13 CC receptor alpha 1 subunit) appearing as ADN62575. Also included are a cector comprising the nucleic acid molecule and a host cell comprising the vector comprising the nucleic acid molecule and a host cell comprising the vector comprising the nucleic acid molecule and a host cell comprising the vector comprising to a lelic variation. The polypeptides are useful for binding the comprision of the vector allelic variation. The polypeptides are useful for binding the number of the interfering with the interaction between human II-13 or II-4 and their contrains receptors. They can also be used in medicine, e.g. for treatment contrains a such as atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and contrains and latendary boxels, psoriasis, thus contrains they contrains and leichmaniasis, ulcerative colitis, contrains, nephrotic syndrome, glomerulonephritis, ulcerative colitis, contrains disease, tuberculosis, malaria and leichmaniasis. They can also be used for producing antibodies, which can be used for diagnosing diseases. They can also be contrained to the present sequence encodes II-13 receptor alpha 1 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule encoding a polypeptide capable of binding human IL-13 and/or binding human IL-4, useful in medicine, in
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GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAGAGCCTAGC
                                                                                                                                                                                                                                                                                                      CGGCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGCGCTCTGCGGGCTGTGG
                                                                             GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAAT
                                                                                                                                                         TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTTGGC
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                                                        GACAAACAAGATAAGAAAATAGCTCCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAAT
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"Mature IL-13 receptor alpha 1 chain"
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New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inhibitor; allergy; allergic disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                     Page 1253-1254; 1343pp; English
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The present invention describes a new composition comprising an antisense coligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, cantiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. is chaemic conditions, pulmonary vascoonstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including threat and prostate cancer. The reduction of the adenosine content of the conchoconstriction and inflammation. AAA32313 to AAA33312 represent the concluding the content of the prochoconstriction and inflammation. nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 18 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 160 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence 185

4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

Query Match Best Local Sim Matches 1348; Similarity Conservative 96.4**%**; 99.6**%**; 0; Score 1333.8; Pred. No. 0; Mismatches DВ 2; ω •• Indels Length 4039; ω '' Gaps

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GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAAGGCTCAAG
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                                                                    CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
                                                                                                                             ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC
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                                                CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
                                                                                                           ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC
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AAF21336 standard; DNA;

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14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence

RESULT 13
AAF21336
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XX AAF21
XX Low a
XW Low a
XW human
XW Inmun
KW respi
KW respi
KW chron
CH Chro
CO Chro
CO Jigc
CC Oligc
CC Oligc
CC Oligc
CC Climmun
CC The F
CC Climmun
CC The Scc
CC Cligc
CC Cligc Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; ss.

sapiens

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020

06-APR-1999; 99US-0127958P

(UYEC-) UNIV EAST CAROLINA.

Low adenosine (A) content antisense oligonuclectides which do no adenosine receptors during metabolism, useful e.g. for treating and respiratory obstructions. not cancers

1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and

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Best Local Similarity
Matches 1348; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide the processor inventions of the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
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                        AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
                                                                                  GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA
                                                                                                                 GTGAAGGATTCCAGTTTTGAACACACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA
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XX ABL67
XX ABL67
XX ABL67
XX Ocsop
XX Human
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KW Stomaa
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05-JUN-2000; 2000US-0209473P.
05-JUN-2000; 2000US-0209531P.
18-SEP-2000; 2000US-0233133P.
18-SEP-2000; 2000US-0233617P.
                                                                                                                                                                                                                                                                                                                                                                                           Oesophagus
                                                                                                           30-MAY-2001;
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL67709;
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                                                                                                                                                                                                WO200194629-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751
                                                                                                                                                                                                                                                                                                                                               cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATTTTTACCTTCACTGTGACCTTGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGAATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGAAATGAGTAAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATATTAAAAACCTCTCCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTATTTTACCTTCACTGTGACCTTGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                           cancer related
                                                                                                             2001WO-US010838
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4039
                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                         carcinoma; and
lastic; Wilm's
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                             antitumour;
                                                                                                                                                                                                                                                                                                                                                                                              NO:6046
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1170

1276 1290 1216 1230 1110

1036 1050 976 990 916 930 856

1096

adenocarcinoma; cancerous;

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The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000
28-SEP-2000
28-SEP-2000
28-SEP-2000
28-SEP-2000
29-SEP-2000
29-SEP-2000
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02-OCT-2000
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02-OCT-2000
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03-OCT-2000
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25-SEP-2000
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26-SEP-2000
27-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young F
Soppet
                                                                                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing agent to be tested for anti-neoplastic activity, and coin expression of a gene of a signature gene set.
                                   Sequence 4039
                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 6046; 44pp; English.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE,
DR,
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2000US-0235637P
2000US-0235720P
2000US-0235843P
2000US-0235863P
2000US-0236032P
2000US-0236033P
2000US-0236034P
2000US-0236034P
2000US-0236119P
2000US-023611P
2000US-023611P
2000US-023611P
2000US-023611P
2000US-0237173P
2000US-023718P
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2000US-0235134P.
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2000US-0234924P.
2000US-0235077P.
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2000US-0234034P
2000US-0234052P
                               BP; 1135 A; 839 C; 896 G; 1169 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter KC,
   Score 1333.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,R
   В
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 6
                               U; 0 Other;
Length 4039
                                                                                                                                                                                                                                                                                                                                                                                                  g cells to a chemical determining a change
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1110	1051 CAAGAAATGAGTAATAGGTAAGAAGCGCAATTCCACACCTCTACATAACCATGTTACTCATT	8
03		B 1
٠ ،	91 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGAACAACTCTGGAGTAATTGAGGAG	O 1
990 976	931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTTGAACACAGTCAGA	g da
916	TTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTG	Db
930	CGI	Qy
856	797 AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA	B &
י נ	COLONDO COLOND	? 8
• ⊢		로 &
736	677 AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA	₽
750	TAACTTCCCGTGTGAAACCTGATCCTC	δ
690	631 GIGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA 	B &
, ,_	57 CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGCTTTTGATCTGAC	} B
630	71 CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGG	Ş
570 556	511 ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAATTCAT	Db Qy
496	437 CTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAA	Db
510	451 CTTCAATGCATTTGGCACAACCTGAAGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAA	Q
436	377 ATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAG	뮹
450	391 ATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAA	8
376	31 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGGTGAGAAGCCTAGC 317 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGC	ß &
	5) GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCCGTTCAATAGAAGTACCCCTGAA) b
w	71 GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAA	\$ 8
256	197 TGGAATCCACCGAGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTGGC	₽ &
9	CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGAC	?
Ĥ	CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGAC	\$ 5
w		Ф
150		δ
93 76	34 CGGCCGGGTTCCGAAGGCGAAAAGCTGGATGAATGGCCGGCGGCGCGCTCTGCGGGCTGTGG	B &
1,	Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps	Ве Ма

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RESULT 15
ABK84753
ID ABK84
XX
AC ABK84
XX
AC ABK84
XX
DT 14-AI
XX
Huma
XX
Huma
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                         Detecting granulocyte activation by detecting genes associated with granulocyte activation,
                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                            Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2000; 2000US-0237189P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2001; 2001WO-US030821.
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                                                                                                                                                                                                                                                                                                                                                                                  2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; parasitic infection; protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC
                                                                                                                                                                                                                                       SEQ ID NO 1324; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTATTTTTACCTTCACTGTGACCTTGAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAACCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentially expressed in
                                                                                                                                                                                                                                                                                        is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Weissman
                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4039
                                                                                                                                                                                                                                                                                 monitoring disease
                                                                                                                                                                                                                                                                                                                                                                                                                              , MS
                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocytic cells #1324.
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CC pathogen or sterile inflammatory disease using the gene expression CC profile; (3) detecting (MA) an inflammation (especially chronic) in a CC tissue, an allergic response in a subject, exposure of a subject to a cxpression in a sample of the tissue of gene(s) from Gs, where the level of cexpression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating CC (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile conflammatory disease, by contacting a tissue having inflammation with an eagent that modulates the expression of gene(s) from Gs in the tissue. MI conflammation in a tissue; M is useful for modulating GA, M3 is useful for screening an agent capable of modulating GCA preferably in an CC (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, conditions in the tissue, an allergic response in a subject, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult creative colities, periodontal disease; also bacterial infection, parasitic infection, protozoal infection, conditions The present sequence represents a gene differentially.
                                                                          conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1
CR603161
LOCUS
DEFINITION ORIGIN FEATURES COMMENT TITLE JOURNAL REMARK Query Match source Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi - Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. full-length cDNA clone C of Homo sapiens (human). CR603161 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Genoscope Faraday Avenue CR603161.1 GI:50483968 CR603161 Hominidae; Homo. Homo sapiens Homo sapiens (human) (bases 1 to 1756) CNSLT_cDNA. /clone="CSODIOO1YN10" /tissue_type="placenta Cot 25-normalized" /plasmid="pCMVSPORT_6" /organism="Homo sapiens"
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/db_xref="taxon:9606" Location/Qualifiers 84.9%; Score 1174; CSODIOOLYN10 1756 bp DB 6; mRNA linea O of Placenta Length 1756; linear Cot HTC 21-JUL-2004 25-normalized

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Email: seqrefegenoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31 Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex -
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AL543336
AL543336.3 GI:45718896
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CTCTGTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTC
                                                            GGGCGGGGGGGGGGCCCGCCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGT
                                                                                     GGCGGGGGGCGGGGG-----CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGT
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/tissue_type="PLACENTA COT 25-NORWALIZED"
/tissue_type="PLACENTA COT 25-NORWALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
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HTC; CAP trapper:
Mus musculus (house mouse
Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                  AK089984 1865 bp mRNA linear HTC 02-SEP-2005 Mus musculus colon RCB-0549 Cle-H3 cDNA, RIKEN full-length enriched library, clone:G430044I06 product:interleukin 13 receptor, alpha 1,
                                                                                                                                                                                                                             CTATGAGGATGACAAACTCTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGA 1072
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prepare mouse tissues.
Please visit our web site for f
URL:http://genome.gsc.riken.jp/
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                               The RIKEN Genome Exploration Research
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Phase I and II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs Genome based Exploration Research 9 functional Group

RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antieense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005) Science Group

The FANTOM Consortium, Riken Genome Exploration Research Genome Science Group (Genome Network Project Core Group). The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)

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Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute c Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute c Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URLihttp://genome.gs.criken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contributed Yokohama (GSC) of. to

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AK082889

Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430004G12 product:interleukin 13 receptor,
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                                                                                                 musculus (house mouse)
                                                                                                               CAP trapper.
                                                                                                                                                                         full
                                                  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                       GI:26350060
                                Muroidea;
Hayashizaki,Y
                                                                                                                                                                       sequence.
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1354 1291 1294 1234 1171 1174 1111 1114

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                                                                                                                                                                                               Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                         Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN Genome Exploration Research Group, Genome Science (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
cDNA library was prepared and sequenced in Mouse Genome
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LTSYVKPDPPHIKHLLQNGALLVOMKAPQNFRSRCLTYEVEVNNTOTDRHNILEVEE
DKCQNSESDRAMEGTSCFPLFGVLADAVYTVKPRVQTNKLCFDDNQLMSDMSEAQSIG
KEPNSTFYTTMLLTIPVFVAVAVIILLFYLRRLKIIIFPPIPDFGKIFKEMFGDQNDD
TLHMKKYDIYEKQSKEETDSVVLIENLKKAAP"
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/db_xref="G1:26350061"
/db_xref="G1:26350061"
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TIIWTMSPPEGASPNCTLRYFSHFDDQQDKKLAPETHRKEELPLDEKICLQVGSQCSA
NESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLYY
NESEKPSPLVKKCISPPEGDPESAVTELKCIWHNLSYMKCSWLPGRNTSPDTHYTLYY
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/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                            Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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                                                                                                                                          Encyclopedia Project of Genome Exploration
Genomic Sciences Center and Genome Science
Division of Experimental Animal Research in
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                          URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
                                                                                             prepare mouse tissues.
Please visit our web site for further details.
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Best Local Similarity
Matches 1100; Conserv
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                                                                                                                          TTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCACATA
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                                                                   TTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAGAATT
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/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A530070009"
/db_xref="taxon:I0090"
/clone="A530070009"
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1. .1677
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GB|S80963, evidence: E
putative"
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/clone_lib="RIKEN full-length enriched
/dev_stage="adult"
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81.2%;
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l. No. 6.1e-235;
fismatches 243;
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3718 bp mRNA linear HTC 21-SEP-2005 Mus musculus MOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630103B18 product:interleukin 13 receptor, alpha 1, full insert sequence.
                                                                                                                                                                                ATTT----
                                                                                                                                                                                                                 ACGGATTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCAGCTCCTTGATGGGGAAGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGCCAAG
                                                                                                                                            ATTTCTTTGCCTTCAATGTGACCCTGTGAAGA
                                                                                                                                                                                                                                     ACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGAGAGATAATTT 1353
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                                                                                                                                                                                                                                                                                   ATGATGATAGCCCTGCACTGGAAGAAGTATGACATCTATGAGAAACAATCCAAAGAAGAA
                                                                                                                                                                                                                                                                                                                    ATGATGATA-CTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAGATTA 1174
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RESULT 6
AK154675
LOCUS
DEFINITION

SOURCE ORGANISM ACCESSION VERSION KEYWORDS HTC; CAP trapper. AK154675 AK154675.1 GI:74185756 musculus (house mouse)

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Mammalia; Eutheria; Euarchontoglires; Sciurognathi; Muroidea; Muridae; Murin Mus musculus Murinae; Mus.

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)

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TITLE
JOURNAL
PUBMED
REFERENCE TITLE AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new greeneme Res. 10 (10), 1617-1630 (2000)

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishin, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Carninci, P.,

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Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aldinis,V., Allen,J.E., Zavolan,M., Davis,M.J., Wilming,L.G., Aldinis,V., Bailey,T.L., Ambesi Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M. Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., Circwe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., Circwe,M.L., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
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                  source
                                                                                      URL:http://genome.gsc.riken.jp/
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Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Submission (Alexander Context (GSC))
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                                      prepare mouse tissues by Dr. John Todd (Dept. of Medical Genetics Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details
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                   ATTT----TTACCTTCACTGTGACCTTGAGAAGA
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ATTTCTTTCTTGCCTTCAATGTGACCCTGTGAAGA
                                                                                                                                                AATGATGATACCCTGCACTGGAAGAAGTATGACATCTATGAGAAACAATCCAAAGAAGAA
                                                                                                                                                                       AATGATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAGGAA
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                                                                          ACGGATTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCAGCTCCTTGATGGGGAGAAGTG
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RESULT 7
AK143292
LOCUS
DEFINITION

21-SEP-2005 RIKEN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM HTC; CAP trapp Mus musculus Mus musculus AK143292 ARNA linear HTC 21-SEP-200: Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:8230035008 product:interleukin interpretation alpha 1, full insert sequence. AK143292 AK143292.1 GI:74226353 CAP trapper.

(house

mouse)

Eukaryota; Metazoa; Cho Mammalia; Eutheria; Eua Sciurognathi; Muroidea; Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; dea; Muridae; Murinae; Mus.

cloning

Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 10349636

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000) 6 genes

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AUTHORS
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forreet, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ringy, B.Z., Ringwald, M.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Walsande, N., Saho, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Hayatsu, N., Hirozane, Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
TM FANTOM Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Labbratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokoha Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                        prepare mouse tissues.
Please visit our web site for further
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science
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Antisense transcription in the mammalian transcriptome
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                                                                                                                                                                                       organism="Mus musculus"
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/tissue_type="oviduct"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="2 days pregnant adult"
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/protein_id="BAE25336.1"
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                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12279 row: p column: 21
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TTCATGGTCCCT-GGTGTTCCTTCCTGATACTTTGAACACAGTCAGAATAAGAGTCAAAAAC
                                               GTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTGGAGAATACATCTTGT
                                                                                                       TGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTAC
                                                                                                                                            TCCTTCCACAATGACCTATATGTGCAATGGGAGAATCCACAGAATTTTATTAGCAGA
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo c
Average insert size 2 kb. Library constructed by Life
Technologies."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2454 row: o column: 05
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1 (bases 1 to 978)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
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High quality sequence stop: 627.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Mammalia; Eutheria;
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                                                            ATAAGGTAGAAAGCGCCAATTCACACTCTACATAAACCT
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/tab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_ll2"
/clone_lib="NIH MGC_ll2"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: bkin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI/ CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G), Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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Euarchontoglires; Primates; Cat
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                                                                                                                           AGENCOURT 13666655 NIH MGC 184 Homo IMAGE:30353391 5', mRNĀ sequence. CB956372 CB956372.1 GI:30212489 EST.
             Hominidae; Homo.
1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    Homo
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90; Conservative
             ACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATG
                                                                        GGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAA
                                                                                                                           TGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAA
                                                                                                                                                                                   GGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTT
                                                                                                                                                                                                                                              TGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTC
ACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATG
                                                      GGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAA
                                                                                                                                                                                                                             CCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCT
                                                                                                                                                                                                                                                                                                     TGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCT
                                                                                                                                                                                                                                                                                                                                             TGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTC
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                                                                                                              TGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAA
                                                                                                                                                                    GGAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTT
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Indels

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Gaps ·

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palko
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM154 row: a column: 16
High quality sequence stop: 651.
Location/Qualifiers
                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                         Note: this is a NIH_MGC Library."
Score 766.2; DB 4;
Pred. No. 7.8e-198;
0; Mismatches 4;
                                   Length
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Origin Query M Best Lo Matches Qy Db Qy	FEATURES SOUTCE	PUBMED PUBMED REFERENCE AUTHORS TITLE TOURNAL COMMENT	REFERENCE AUTHORS TITLE JOURNAL	DQ034842 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	D	00 DB QV DB QV QV
Query Match Ouery Match S3.5%; Score 739.4; DB 14; Length 866; Best Local Similarity 88.6%; Pred. No. 1.7e-190; Matches 740; Conservative 0; Mismatches 95; Indels 0; Gaps 0; 146 AAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGGACAGTAATAT 205	Q	15869325 2 (bases 1 to Nielsen,R., Bus Hubisz,M.J., Fl White,T.J., Sni Direct Submissi Direct Submissol Submitted (05-M Rockville, MD 2 This sequence w them based on a	1 (bases 1 Nielsen,R., Hubisz,M.J. White,T.J., A Scan for Chimpanzees (er) PLOS E	- ·	977 TGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGATGACAAACTC 1035	798 GGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAG 857
REFERENCE AUTHORS TITLE JOURNAL PUBMED	DOS 4843 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	QY QY dd	Db Qy Db	B & B & B &		Q D D Q Q D Q Q D D D D D D D D D D D D
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 729) 1 (bases 1 to 729) 1 (bases 1, to 729) 2 (bases 1, to 729) 3 (bases 1, to 729) 3 (bases 1, to 729) 4 (bases 1, to 729) 5 (bases 1, to 729) 5 (bases 1, to 729) 6 (bases 1, to 729) 6 (bases 1, to 729) 7 (bases 1, to 729) 8 (bases 1, to 729) 1 (bases 1, to 729) 2 (bases 1, to 729) 2 (bases 1, to 729) 2 (bases 1, to 729) 3 (bases 1, to 729) 4 (bases 1, to 729) 1 (bases 1, to 729) 2 (bases 1, to 729) 2 (bases 1, to 729) 2 (bases 1, to 729) 3 (bases 1, to 729) 4 (bases 1, to 729) 2 (bases 1, to 729) 2 (bases 1, to 729) 3 (bases 1, to 729) 4 (bases 1, to 729) 5 (bases 1, to 729) 6 (bases 1, to	02-JU	866 AGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAGAATCCAGAATTTGAGAGAA 925	746 CTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATC 805	566 TTCATCAATGTGAAAACATCTTTTAGAGAAAGGCCAATACTTTGGTTGTTTGT	CTAGCATTTTGGTTGAAAATGCATCTCTACTATTGGCACAGAAGCCTGGAAAAAAAA	

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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was made by sequencing genomic them based on alignment. Translation starts
                                                                                                                                                                                                                                                                                                                                                         GAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAAGTGAAG 636
                                                                                                                                                                                                            AAACCATCCTTCAATATAGIGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCACATATT
                                                                                                                                                                                                                                                                              GATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGAAAAATT
                                                                                                                                                                                                                                                                                                                                  GAĀĀĀCĀTCTATĀĞNNNNNGCCAĀTĀCTTTĞĞTTĞTTCCTTTĞĀTCTĞACCAĀAGTGAĀG
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     GTTTTCTAC
                                                         ATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAAT
                                                                                                                                                AAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAGAATTTT
                                                                                                                                                                                   AAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCACATATT
                                                                                                                                                                                                                                                           GATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                            CCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAATTCATCAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAACTTĆAA 456
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/mol_type="genomic DNA"
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10702 row: d column: 14
High quality sequence stop: 755.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602678850F1 NIH_MGC_95 Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                     CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA
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TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTTGGC
                                                                                                        CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTGCACAGTAATATGGACA
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//clone_lib="NIH_MGC_95"
//note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI [gtcgag]; Oligo-dT primed using primer for average for the following primer for the following primer for the following primer for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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/lab_host="DH10B"
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Consortium (LLNL)

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                                                                                                                        Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 16363365 NIH MGC 221 Homo IMAGE:30708826 5', mRNA sequence CKOnna4'
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National Institutes of Health, Mammalian
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1 (bases 1 to 842)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                               quality sequence stop: 681.
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/mol_type="mRNA"
                 organism="Homo sapiens"
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/(clone lib=NIH MCC_221"
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Site 2: NotI; Library is oligo-dT primed and directionally cloned benatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with size selected according tomRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 4-5Kb. Adaptors 5'(AATTCGGCAGGAGG)3' and 5'd (CCTCGTGCCG)3'. 3' Linker sequence - GCGCCGCTGAGAGGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTAACGCTCACTAAAGGGA)3'. Library was constructed in the labour that the AMADGCTCACTAAAGGGA)3'. Library was constructed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:30708826"
/lab_host="DH10B_TonA"
laboratory of M. Bento Soares. Note: this is a NIH_MGC
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729 CCGTGTGAAACCTGATCCTCCACATATTAAAAAACCTCTCCTTCCACAATGATGACCTATA
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AGCCTCTCAGTGATGGAGATAATTTATTTTTACCTTCACTGTGACCCTTGAGAAGA 1383
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Best Local Similarity
Matches 632; Conserv
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Seq primer: M13RP1 reverse primer
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: graeme@helix.nih.gov
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Fax: 301 496 0078
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Mol. Vis. 8 (4), 205-220 (2002)
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CA391344
CA391344.1 GI:24723148
EST.
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                     AGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAG 377
                                                                                      TAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGA 180
                                                                                                                     TAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGA 317
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-(http://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the Notl/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified); cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="EMDH10B"
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99.8%;
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Pred. No. 5.5e-161;
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ACATA	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	AGTG! - - - AGTG!	TCAAT	TACCA	ACTTO	CATTI
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Search completed: July 7, 2006, 23:51:33 Job time: 6251 secs

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1: PMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*
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GGCGGGGGCGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCT

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Qy 1 GAGT	Query Match Best Local Similarity Matches 1383; Conser	RESULT 1 US-09-688-286D-3 Sequence 3, Application US/0 Patent No. 6911530 GENERAL INFORMATION: APPLICANT: Willson, Tracey APPLICANT: Willson, Douglas APPLICANT: Hilton, Douglas APPLICANT: Hilton, Douglas APPLICANT: Lahng, Jian ITITLE OF INVENTION: A novél PILE REFERENCE: 23199-215 CURRENT APPLICATION NUMBER: A PRIOR FILING DATE: 1995-10- PRIOR APPLICATION NUMBER: A PRIOR FILING DATE: 1995-12- PRIOR FILING DATE: 1995-12- PRIOR FILING DATE: 1996-09- NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATORE: LANG SEQ ID NO SEQ ID NA ORGANISM: human FEATURE: NAME/KEY: CDS LOCATION: (61)(1338) OTHER INFORMATION: US-09-688-286D-3		C 254 25 24 25 26 26 26 26 26 26 26 26 26 26 26 26 26
GAGTCTAACACGGACCAAGGAGT GAGTCTAACACGGACCAAGGAGTT	100.0%; 100.0%; vative 0;	ion US/09 Tracey , Nicos , Nicos Douglas , Donald Jian A novel 99-215 NUMBER: AU 10MBER: AU 10MBER: AU 11995-12-2 UMBER: AU 11995-12-2 UMBER: AU 11995-12-2 UMBER: AU 11995-13-2 Version 3		3.3 1345 2 US- 3.3 1368 2 US- 3.3 1808 2 US- 3.3 1808 2 US- 3.3 1808 2 US- 3.3 1808 2 US-
GAGTCTAACACGGACCAAGGAGTTTAACACGTGCGGCCGGGTTCCGAGGCGAGAGGCTGC 	Score 1383; DB 3; Pred. No. 0; Mismatches 0;	688286D haemopoietin receptor and US/09/688,286D 17-10 17-10 17-10 17-10 17-10 17-10 17-10 18-19 19-10	ALIGNMENTS	-09-806-708B-22 -07-757-390-3 -08-442-281-3 -08-442-281-3 -08-442-282-1 -08-442-282-1 -08-442-282-1 -07-757-390-4 -07-757-390-4 -08-442-282-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-1 -08-442-281-2 -08-442-282-2 -07-757-390-1 -08-442-282-2 -08-442-282-1 -08-442-282-1
TTCCGAGGCGAGAGGCTGC 60	Length 1383; Indels 0; Gaps 0;	d genetic sequences encoding		Sequence 22, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 16, Appli Sequence 2, Appli

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GGCAAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAG
                                                GTACTCCTGCTTTACCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCT
                                                                     TCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATA
                                                                                                                                                                                                 GAGGATGACAAACTCTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAAT
                                                                                                                                                                                                                                                                       GTTCTTCCTGATACTTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTAT
                                                                                                                                                                                                                                                                                                                                             TGTGAGAATCCAGAATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGT
                                                                                                                                                                                                                                                                                                                                                                   TGTGAGAATTCCAGAATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGT
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                                                                                                                          TCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCAAATAATGGTCAAGGATAATGCAGGAAAAATTAAAACCATCCTTCAATATAGTGCCT
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GENERAL INFORMATION:
APPLICANT: NYCE, Jor
TITLE OF INVENTION:
                                                                                                      Matches 1348;
                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2902: SEQUENCE CHARACTERISTICS: LENGTH: 3999 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSE: EPIGENESIS PHARMACEUTICALS,
STREET: 7 Clarke Drive
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                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: N/A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                        94
                                                                 34 CGGCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGGCGCCTCTGCGGGCTGTGG
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            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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COUNTRY: USA
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cranbury
                                                                                                                                                                                                                                                                                 TELEFAX: 413-254-9245
                                                                                                        Conservative
                                                                                                                   96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09543679A
                                                                                                      0
                                                                                                      Score 1333.8;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT 1110
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CAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG 1290
                                                                                                   ATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAdAC 1230
                                                                                                                                                                                                                                                                                                                               CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1050
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                                                                                                                                                                                             GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAAGGCTCAAG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1026
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS

LOCATION: 43..1323

SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ
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US-08-969-125-8
US-08-969-125-8
; Sequence 8, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
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Best Local Similarity 99.6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125B
FILING DATE: 12-No. 6143871-1997
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: FRAGMENT TYPE:
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ADDRESSEE: NIXON & VANDERHYE
STREET: 1100 NORTH GLEBE ROAD
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GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
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                                                                                                                                                                                                    GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA 1350
                                  LENGTH: 4038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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linear
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CAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG
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                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1348; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4038 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/545,002
FILING DATE: 12-No. 6743604-1997
CLASSIFICATION LONGER: US/08/969,125
APPLICATION NUMBER: US/08/969,125
FILING DATE: 12-No. 6743604-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NUMBER: WITGON MADEY

APPLICATION OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1
MOLECULE TYPE: 1
FRAGMENT TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1336
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ADDRESSEE: NIXON &
STREET: 1100 NORTH
CITY: ARLINGTON
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GAUCHAT, JEAN-FRANCOIS
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                                                                                                                                                       GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA
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NAME/KEY:
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STRANDEDNESS: single
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TELEFAX: (703) 816-4100
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 4039
TYPE: DNA
ORGANISM: Human
US-09-949-016-223
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US-09-949-016-223
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Best Local Similarity
Matches 1348; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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RESULT 6
US-09-880-107-3856
Sequence 3856, Application US/0
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Genba
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CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-05-14
PRIOR FILING DATE: 2000-10-02
NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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RESULT 7

US-09-543-679A-2903

US-09-543-679A-2903

; Sequence 2903, Application US/UJJ...
; Sequence 2903, Application US/UJJ...
; Patent NO. 7034007
; GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
APPLICANT: NYCE,
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS,
STREET: 7 Clarke Drive
                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: N/A
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                       APPLICATION NUMBER: 60/127,958 FILING DATE: 1998-08-03 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                     CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
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Best Local Similarity
Matches 1348; Conser
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INFORMATION FOR SEQ ID NO: 2903:
SEQUENCE CHARACTERISTICS:
LENGTH: 4039 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
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AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA
                                                                                     CATATTAAAAACCTCTCCCTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
                                                                                                                                                                    AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
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Pred. No. 0;
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Query Match Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1; Qy 34 CGCCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCGGCGCGCGC	; SEQ ID NO 5 ; LENGTH: 11927 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-193-707-5	FILE OF INVENTION: A PREDETERMINED PROPERTY FILE REFERENCE: 8358-0005-999 CURRENT APPLICATION NUMBER: US/09/193,707 CURRENT FILING DATE: 1998-11-17 NUMBER OF SEQ ID NOS: 18 SOFTWARE: FastSEQ for Windows Version 3.0	; APPLICANT: Orberger, Georg H. ; APPLICANT: Koller, Daniel ; APPLICANT: Bailey, James E. ; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY, ; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WI	; Sequence 5, Application US/09193707 ; Patent No. 6524792 ; GENERAL INFORMATION: ; APPLICANT: Renner, Wolfgang A.	SULT 8	1351 TITATTITTACCTTCACTGTGACCTTGAGAAGA 1383	1291 GAAACCGACTCTGTAGTGCTGATAGAAAAACCTGAAGAAAGCCTCTCAGTGATGAGATAA 	Qy 1231 CAGAATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG 1290	Qy 1171 ATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC 1230		Qy 1051 CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT 1110	Qy 991 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC 1050	Qy 931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGGTCAGA 990	Qy 871 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATTTGAGAGAAATGTG 930	Db 797 AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA 856
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CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA		GGCTGCATGGAGTGGCCGGCCGCGCTCTGCGGGCTGTGG 93	Query Match 96.4%; Score 1333.8; DB 5; Length 14978; Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;	; STRANDEDNESS: single ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 2905: US-09-543-679A-2905	; INFORMATION FOR SEQ ID NO: 2905: ; SEQUENCE CHARACTERISICS: ; LENGTH: 14978 base pairs ; TYPE: nucleic acid	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 609-409-3035 ; TELEFAX: 413-254-9245 ; TELEX: <unknown></unknown>	; ATTORNEY/AGENT INFORMATION: ; NAME: Amzel, Viviane; ; REGISTRATION NUMBER: 30,930 ; REFERENCE/DOCKET NUMBER: EPI-0067191b	CLASSIFICATION: UNKNOWN PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/127,958 FILING DATE: 1998-08-03	; SOFTWARE: N/A ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/543,679A ; FILING DATE: 13-Apr-2000	; COMPUTER READABLE FORM: ; MEDIUM TYPE: CD-R ; COMPUTER: IBM Compatible ; OPERATING SYSTEM: DOS	5 · · · Z · R		ON: LOW AI COMPOS OF AIR BRONCH	; Sequence 2905, Application US/09543679A ; Patent No. 7034007 ; GENERAL INFORMATION: ; APPLICANT: NYCE, Jonathan W.	RESULT 9 US-09-543-679A-2905	Qy 1351 TTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1383	Qy 1291 GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGAAGAATAA 1350 	Qy 1231 CAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAG 1290
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SEQ ID NO 49
LENGTH: 1547
TYPE: DNA
ORGANISM: Canis familiaris
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APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine
APPLICANT: Tang, Liang A.
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OTHER INFORMATION:
-09-828-995B-49
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NAME/KEY: CDS
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CURRENT APPLICATION NUMBER: US/09/828,99
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                 Sequence 51, Application Patent No. 6703360 GENERAL INFORMATION:
                                                                                                                                   APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                        FILE REFERENCE: AL-7
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

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16 US-10-671-697-8

10 US-09-962-832-160

10 US-09-880-107-3856

7 US-10-172-118-633

10 US-10-342-887-633

10 US-10-342-887-633

10 US-10-843-641A-6046

10 US-10-850-698-50

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Sequence 3, Appli
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Sequence 633, Appli
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69.4 69.4	69.4	71.1	71.1	71.1	71.1	72.9	72.9	72.9	72.9	72.9	73.0	73.0	73.0	73.0	73.0	73.1	73.1	73.1	73.1	73.1	73.2	73.2	73.2	73.2	73.2	73.2
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*ENGTH: 1383
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                                                                                                                              Query Match 99.5%;
Best Local Similarity 99.7%;
Matches 1379; Conservative
                                                                                                                                                                                                                                                        LENGTH: 1383
TYPE: DNA
ORGANISM: Human 3
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APPLICANT: Nicola, Nicos A.
APPLICANT: Hilton, Douglas J.
APPLICANT: Hilton, Douglas J.
APPLICANT: Metcali, Donald
APPLICANT: Zhang, Jian G.
TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
TITLE OF INVENTION: ENCODING SAME
FILE REFERENCE: Davies cc
CURRENT APPLICATION NUMBER: US/10/036,568
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US/09/051,843
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(1338)
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Sequence 3, Application US/11185230
; Deblication No. US20050282216A1
; GENERAL INFORMATION:
   APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
APPLICANT: Laurent, Patrick
; APPLICANT: Laurent, Patrick
; APPLICANT: Lide, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 3
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity
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Pred. No. 0;
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RESULT 3
US-11-182-384A-3
; Sequence 3, Application US/11182384A
; Publication No. US20060035855A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
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Best Local S
Matches 1348
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                                                                                                                                                                    CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAA
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  AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA
                                                                             AAAATTAAACCATCCATTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA
                                                                                                                                                                                                                ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCCTGGAAAAAAATTCAT
                                                                                                                                                                                                                                                                                                        ATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                 GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTTCGATAGAAGTACCCCTGAAT
                      CATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
                                                                                                                                                        CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGCTTTGATCTGACCAAA
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99.6%;
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; TITLE OF INVENTION: Purified polypeptides having IL-
; FILE REFERENCE: IVD924 US DIV 2
; CURRENT APPLICATION NUMBER: US/11/182,384A
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 09/077,817
PRIOR APPLICATION NUMBER: 09/077,817
PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Homo sapiens
CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA
                                                                                                                                          GCCTGCTCTGCGCCGGCGGCGGGGGGGGGGGGGGGGGGCGCCCTACGGAAACT
                                                                                                                                                              CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA
                                                                                                                                                                                                               CGGCCGGGCTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGCGCCTCTGCGGGCTGTGG
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Pred. No. 0;
0; Mismatches
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	QY 34 CGCCGGGTTCCGAGGCGAGGCTGTAGGTGGCGGCGCGCGC
1027 CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTAC 1111 GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGGC	Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps
1051 CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT	A-3 96.4%; Score
991 ATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGC	LENGTH: 400 TYPE: DNA ORGANISM: H
931 GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGA	PRIOR FILING DATE: 1996-1: NUMBER OF SEQ ID NOS: 15 SOFTWARE: PatentIn version SEO ID NO 3
871 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTG	CURRENT FILING DATE: 2005-07-15 PRIOR APPLICATION NUMBER: 09/077,817 PRIOR FILING DATE: 1998-09-14 PRIOR APPLICATION NUMBER: PCT/FR96/017
811 AATTITATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA	APPLICAN TITLE OF FILE REF
751 CATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG 	GENERAL INFORMATION: APPLICANT: Caput, Daniel APPLICANT: Ferrara, Pascual APPLICANT: Laurent, Patrick
691 AAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA 	RESULT 4 US-11-183-599A-3 ; Sequence 3, Application US/11183599A ; Publication No. US20060035856A1 Db
631 GTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGA	1327 TTTATTTTTACCTTCACTGTGACCTTGAGAAGA
571 CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGCTTCCTTTGATCTGACCAAA 	
511 ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCAT 	
451 CTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAA	
391 ATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAA	
331 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGC 	1027 CANGAATGAGTATAGGTAAGAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAG
271 GACAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAAT 	967 ATBAGAGTCAAAACAATAAGTTATGCTATGAGATAACCATGTTACTCATT
211 TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCATTTTGGC	991 ATAAGAGTCAAAACAAATAAGTTATGCTTATGAGGATGACAAACTTTGGAGGTATTGGAGGA
151 CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA	847 CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAATGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAGAATGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAGAGAAATGAAAATGAGAAATGAGAAATGAGAAAATGAAAATGAGAAATGAGAAATGAGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAAAA
94 GCGCTGCTGCTCTGCGCCCGGCGGGGGGGGGGGGGGGG	Db 787 AATTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA 846 Db 871 CATAATGTTTCTACGTCCAAGAGGCTAAATGTGAGAATTCCAGAATTTTGAGAGAAATGTG 930

Query Match 96.4%; Score 1333.8; DB 8; Length 4038; Best Local Similarity 99.6%; Pred. No. 0; Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1; Qy 34 CGGCCGGGTTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCTCTGCGGGCTCTGCG	MOLEC FRAGM FEATU SEQUE S-10-671-697-	INFORMATIC SEQUE	PRIOR APPLICATION NUMBER: US/10/671,697 FILING DATE: 29-Sep-2003 CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: US 09/545,002 FILING DATE: 06-APR-2000 APPLICATION NUMBER: US 08/969,125</unknown>	COUNTRY: U.S.A. ZIP: 2201-4714 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD COMPUTER: ADDI SYSTEM: MS-DOS	APPLI TITLE NUMBE CORRE	ESULT 5 S-10-671 Sequenc Publica GENER	
\$ \$ \$ \$ \$ \$	D Q D Q	2 2 2 2 4)	оу Оу Оу	0y 0y	ОУ ОУ ОО	D
1051 CAAGAAATGAGTATAGGTAACAAGGGCAATTCCACACTCTACATPACCATGTTACTCATT 1110 1036 CAAGAAATGAGTATAGGTAACAAGGGCAATTCCACACTCTACATAACCACGATTACTCATT 110 1036 CAAGAAATGAGTATAGGTAAGAAGGCGCAATTCCACCACTCTACATAACCATGTTACTCATT 1095 1111 GTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAG 1170 1111	GAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGA	ARITITATIAGE CATAATITTATGAAGTAGAATCCAGAATTGAGAGAATGTGAGAAATTTCAGACAGCCAAACTGAGACACAGACAG	AAAATTAAACCATCCTTCAATATAGGCCTTTAACTTCCCGTGTGAAACCTGATCCTCCA	CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGCTTCCTTTGATCTGACCAAA	451 CTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGAAGGAA	331 GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAAGCGTAAGCCTAGC 390	151 CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA 210

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APPLICANT: Ebher, Reinhard
TITLE OF INVENTION: Cancer Gene Determinatio
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.0
SEQ ID NO 160
LENGTH: 4039
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Best Local Similarity
Matches 1348; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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                                                                                      GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAAGCCTAGC
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                                                                                                                                                                                                                                                                                                  TGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTTAGTCATTTTTGGC
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                                                CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACA
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   ACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCAT
                                                                                                                                                     GAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGC
                                                                                                                                                                                                                GACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCG
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US-09-880-107-3856
; Sequence 3856, Application
; Patent No. US20020142981A1
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                                                                                                                     GENERAL INFORMATION:
            APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENCIN Ver. 2.1
SEQ ID NO 3856
PENCIPH: 4039
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Best Local S
Matches 1348
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ORGANISM: Homo sapiens
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             AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACA
                                                                CATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
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                                                                                                                                                                                                       CAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAA
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                                                  CATATTAAAAACCTCTCCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAG
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APPLICANT: Mac, Mac, Mac, Applicant: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Wan 't Veer, Marc
APPLICANT: Bernards, Rene
ITILE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 930-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 633
LENGTH: 4039
TYPE: DNA
ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 001560
DATABASE ENTRY DATE: 2001-06-18
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US-10-172-118-633
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Best Local Similarity
Matches 1348; Conserv
                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 633, Appropriate Publication No.
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
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 Conservative
              96.4%;
Score 1333.8;
Pred. No. 0;
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US-10-342-887-633

Sequence 633, Application US/10342887

Publication No. US20040058340A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: Linsley, Peter S.

APPLICANT: Mao, Mao

APPLICANT: Wan, Mao

APPLICANT: Van 't Veer, Laura Johanna

APPLICANT: Van 't Veer, Marc J.

APPLICANT: Wan 't Veer, Marc J.

APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of FILE REFERNCE: 9301-188-999

CURRENT APPLICATION NUMBER: US/10/342,887

CURRENT FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: 60/298,918

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PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 10/172,118

PRIOR APPLICATION NUMBER: 10/172,118

PRIOR APPLICATION NUMBER: 50/208,710

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 10/172,118

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PRIOR APPLICATION NUMBER: 10/172,118

PRIOR FILING DATE: 2002-06-14

SEQ ID NO 633

LENGTH: 4039

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Best Local Similarity 99.6%;
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US-10-843-641A-6046
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PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR APPLICATION NUMBER: US/09/964,768
PRIOR PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
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Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
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Best Local Similarity
Matches 1348; Conserv
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TYPE: DNA
ORGANISM: Homo
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Pred. No. 0;
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RESULT 11

US-09-971-392-58

Sequence 58, Application US/09971392

Publication No. US20030134283A1

GENERAL INFORMATION:

APPLICANT: Peterson, David P.

APPLICANT: Pearson, Cecelia I.

APPLICANT: Cocks, Benjamin G.

TITLE OF INVENTION: GENES REGULATED IN

FILE REFERENCE: PA-0029 US
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CCURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/237,652
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PERL Program
SEQ ID NO 58
LENGTH: 4466
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Template ID: 331428.2
NAME/KEY: unsure
LOCATION: 1874-2179, 4212, 4229, 4239, 4
OTHER INFORMATION: a, t, c, g, or other
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Matches 1348; Conserv
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Query Best Match Qy Db Db	RESULT 12 US-10-278-69 Sequence 6 Publicatio Publicatio GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF FILE REFE CURRENT A CURRENT F I CURRENT OF SOFTWARE: SOFTWARE: SEQ ID NO LENGTH: TYPE: DN ORGANISM	D	94 94 95	D Q D Q	B & B &	04 AG AG
Query Match Query	RESULT 12 US-10-278-698-6 US-10-278-698-6 Sequence 6, Application US/10278698 Publication No. US20050037344A1 GENERAL INFORMATION: APPLICANT: PathoArray GmbH APPLICANT: Stuhlmuller, Bruno APPLICANT: Stuhlmuller, Bruno APPLICANT: Haupl, Thomas TITLE OF INVENTION: Nucleic Acid Array PILE REFERENCE: 030027US CURRENT APPLICATION NUMBER: US/10/278,698 CURRENT FILING DATE: 2002-10-23 NUMBER OF SEQ ID NOS: 1050 SOFTWARE: PatentIn version 3.2 SEQ ID NO 6 LENGTH: 1572 TYPE: DNA ORGANISM: Homo sapiens	1291 GAAACCGACTCTGTAGTGCTGATAGAAACCTGAAGAAGCCTCTCAGTGATGAGATAA 1350	1171 ATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGÁC 1230	1051 CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACCACTCTACATAACCATGTTACTCATT 1110		AATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGÁCA
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APPLICANT: SathoArray GmbH
APPLICANT: Stublandler, Bruno
APPLICANT: Stublandler, Bruno
APPLICANT: Haupl, Thomas
ITILE OF INVENTION: Nucleic Acid Array
FILE REFERENCE: 030027US
CURRENT APPLICATION NUMBER: US/10/278,698
CURRENT FILLING DATE: 2002-10-23
NUMBER OF SEQ ID NOS: 1050
SOFTWARE: PatentIn version 3.2
SEQ ID NO 520
LENGTH: 1572
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-278-698-520; Sequence 520, Applica
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Sequence 3, Application US/10850270
Publication No. US20050058645A1
GENERAL INFORMATION:
APPLICANT: AMRAD Operations Pty Ltd (for APPLICANT: Dunlop, Felicity (US only)
APPLICANT: Baca, Manuel (US only)
APPLICANT: Mash, Andrew (US only)
APPLICANT: Fabri, Louis (US only)
APPLICANT: Novention: Novel peptides
FILE REFERENCE: 12175890/E0H
CURRENT APPLICATION NUMBER: US/10/850,270
PRIOR APPLICATION NUMBER: AU PS1301
PRIOR FILING DATE: 2004-05-20
PRIOR FILING DATE: 2002-03-22
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PRIOR FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1284
TYPE: DNA
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                                      GATGACCTATATGTGCAATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTAT
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                                                                                CCTTTAACTTCCCGTGTGAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAAT
                                                                                              CAATACTTTGGTTGTTCCTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACAC
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APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steven H.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOV
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 3880
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-822-846-109
US-09-822-846-109
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1223	4 GCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTT	Qy 116
1163 1021	4 ACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAG	Qy 110 Db 96
1103 961	4 TTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACCTCTACATAACCATGTT	Qy 104 Db 90
1043 901	4 AGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAA 	Qy 98 Db 84
983 841	4 AAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACAC	Qy 92 Db 78
923 781	4 TGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAG	Qy 86 Db 72
863 721	* TCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAÀC 	Qy 80 Db 66
803	TCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAA 	Qy 744 Db 602
743 601	TGCAGGAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGA 	Qy 684 Db 542
683 541	4 GACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATÀA	Qy 62 Db 48
623 481	4 AATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTGTTTGATCT 6	Qy 56. Db 42.
563 421	4 AAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAA	Qy 50 дb 36
361	4 GACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGG 5	Qy 444 Db 302
143 301	GCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGT 4	Qy 384 Db 242
383	CCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAA 3	Qy 324 Db 182
323 L81	TTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACC 3 	Qy 264 Db 122
263	ATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCA 2 	Ду 204 Db 62
203	GGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAAT 2	Qу 144 Db 2
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QY 1284 CAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCCTGAAGAAAGCCTCTCAGTGATG 1343
1082 TGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAAC 1141
Y 1224 TGGAGACCAGAATGATACTCTGCACTGGAÁGAAGTACGACATCTATGAGAAGCAAAC 1283
1022 GCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTT 1081

Search completed: July 7, 2006, 23:03:36 Job time : 1705 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-218-305-11663
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107923,
          2328, Ap
21352, A
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294949,	12119, /	14304, /	32299, F	20981, A	11785, A	24893, A	29031, A	29032, A	450219,	388660,	366840,	2790, Ap	20855, A	16740, A	3379, Ag	311, App	3616, Ap	56474, A	12006, A	481838,

ALIGNMENTS

RESULT 1 US-11-266-748A-25722

GENERAL INFORMATION:

APPLICANT: Harkin, APPLICANT: Johnst APPLICANT: Mullig

Harkin, Paul Johnston, Patrick Mulligan, Karl Sequence 25722, Application US/11266748A Publication No. US20060134663A1

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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
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PRIOR APPLICATION NUMBER: US 60/700,293
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; ORGANISM: Homo Sapiens
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Best Local Similarity 99.6
Matches 1348; Conservative
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ATTATTATATTCCCTCCAATTCCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGAC
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                                                                                                                                     CAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATT
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Paurick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology
CURRENT APPLICATION MUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0410549.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
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Best Local Similarity 99.6%;
Matches 1348; Conservative
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SEQ ID NO 56241
LENGTH: 4006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo
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; Pred. No. 0; 
0; Mismatches
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                                                                                                                        GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA 1350
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                               TTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1383
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                                                                                                GAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGGAGATAA
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FITTLE OF INVENTION: Methods of Using the Same
FITTLE OF INVENTION: Methods of Using the Same
FITTLE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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NAME/KEY: misc_feature
LOCATION: (2177)...(2186)
OTHER INFORMATION: n is
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US-11-266-748A-185183
; Sequence 185183, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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SEQ ID NO 185183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1014;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2741
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1520)..(1834)
OTHER INFORMATION: n is a,
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APPLICANT: Johnsto
APPLICANT: Mulliga
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Mulligan, Karl
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Pred. No. 3e-289;
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Length 2741; Indels

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Sequence 5465, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Malligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Tech
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UNMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-54658
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60) \( \). (60)
; OTHER INFORMATION: n is a
US-11-266-748A-54658
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PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOPTWARE: PatentIn version 3.3
SEQ ID NO 54658
LENGTH: 1016
TYPE: DNA
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                  TGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGC
                                                                                                         GCCTTTAACTTCCCGTGTGAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAA
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Pred. No. 8.8e-280;
3; Mismatches 12;
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Uging the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
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US-11-266-748A-192679
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Best Local Similarity
Matches 973; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version SEQ ID NO 192679
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FILING DATE: 2005-07-18
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
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      GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA
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Pred. No. 4.5e-278;
0; Mismatches 1;
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT, APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.7
PRIOR APPLICATION NUMBER: EP 04105483.7
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-226550
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                                                                                                                                                                                                                                                                                                                            Sequence 226550, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: D. PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: ED 04105484.2

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PAtentin version 3.3

SEQ ID NO 226550

LENGTH: 975

TYPE: DNA

ORGANISM: Homo Sapiens

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Local Similarity 99.9%;
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Pred. No. 4.5e-278;
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APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 04105484.2
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LOCATION: (30)...(30)
OTHER INFORMATION: n is
US-11-266-748A-73628
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 73628
LENGTH: 1294
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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                       CTGGAAGGAATACCAGTCCCGACACTAACTATACTCTC-TACTATTTGGCACAGAAGCCTG
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Sequence 107924, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Willigan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6
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; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; PATURE: misc feature
LOCATION: (30)...(30)
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OR APPLICATION NUMBER: EP 04105483.4
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105507.0
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105485.9
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105484.2
OR FILING DATE: 2004-11-03
OR FILING DATE: 2004-11-03
OR FILING DATE: 2005-03-14
OR APPLICATION NUMBER: US 60/662,276
OR FILING DATE: 2005-07-18
OR APPLICATION NUMBER: US 60/700,293
OR APPLICATION NUMBER: US 60/700,293
OR FILING DATE: 2005-07-18
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                                                                              CCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATTCCAGAATT
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Sequence 126439, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

ITTLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR REPLICATION NUMBER: EP 04105483.4

PRIOR REPLICATION NUMBER: EP 04105483.9

PRIOR REPLICATION NUMBER: EP 04105484.9

PRIOR FILING DATE: 2004-11-03

PRIOR REPLICATION NUMBER: EP 04105484.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-07-18

PRIOR PRIOR FILING DATE: 2005-07-18

PRIOR PRIOR FILING DATE: 2005-07-18

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US-11-266-748A-126439
                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (1265)..(1265)
COTHER INFORMATION: n is a
US-11-266-748A-126439
                                                                                         Query Match
Best Local Similarity
Matches 990; Conserv
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    RESULT 10
US-11-266-748A-54614
Sequence 54614, App.
Publication No. US20
GENERAL INFORMATION
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APPLICANT: Johnst
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Sequence 54614, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick
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Best Local Similarity
Matches 612; Conserv
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TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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NAME/KEY: misc_feature
LOCATION: (872)..(872)
OTHER INFORMATION: n is
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FILING DATE: 2005-03-14
APPLICATION NUMBER: US 60/700,293
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                     TCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATGATACTCTGCA
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                                                                                                 TGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAGATTATTATATTTCCCCTCCAAT 1190
                                                                                                                                             GAAGCGCAATTCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCAGG
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TCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACTCTGCA
                                                                       TGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAGATTATTATATTCCCTCCAAT
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Pred. No. 7.6e-168;
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: US 60/662,276
PRIOR PELICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILLING DATE: 2005-03-14
PRIOR PILLING DATE: 2005-07-18
PRIOR PILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR APPLICATION NUMBER: EP 04105507.0
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NAME/KEY: misc_feature
LOCATION: (60)...(60)
LOCATION: n i
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LOCATION: (180)...(180)
OTHER_INFORMATION: n is
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LOCATION: (174)...(174)
OTHER_INFORMATION: n is
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OTHER INFORMATION: n is
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TYPE: DNA
                    NAME/KEY: misc feature LOCATION: (184)..(184)
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
                                                                                                                                                                                                                                                                                                           Sequence 107923, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 346; Conserv
                                                                                                                                                                                                             APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                              FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NAME/KEY: misc feature
רבייתידוסN: (1011)..(1121)
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LOCATION: (1133)..(113)
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OTHER INFORMATION: n is
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Pred. No. 1.3e-88;
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                                                                                                                                                                                                                     NAME/KEY: misc feature; LOCATION: (1142)...(1187); OTHER INFORMATION: n is US-11-266-748A-107923
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version SEQ ID NO 107923 LENGTH: 1297
                                                                                                                                                             Matches 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR EILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (1138)..(1140) OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (1133)...(1133) OTHER INFORMATION: n is
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LOCATION: (1125)..(1125)
OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (184)..(184)
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OTHER INFORMATION: n is
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OTHER INFORMATION: n
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                                                              1096 ACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTAC
                                                                                                                   1037 GGAGTAATTGGAGCCAAG-AAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTTACATA
                1156 CTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAA
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Gaps

1095 257

1215

Copyright

GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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geneseqn2003bs:*
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Abd20879 Human pul	ABD20879	11	4039	86.6	1198	18
Abz97030 Human nuc	ABZ97030	10	4039	86.6	1198	17
Abn97361 Gene #385	ABN97361	σ	4039	86.6	1198	16
Abk84753 Human cDN	ABK84753	σ	4039	86.6	1198	15
Abl67709 Oesophagu	ABL67709	σ	4039	86.6	1198	14
Aaf21336 Human low	AAF21336	w	4039	86.6	1198	13
Aaa35214 Human ade	AAA35214	w	4039	86.6	1198	12
Adn62574 Human cDN	ADN62574	12	4038	86.6	1198	11
Adl71811 Human int	ADL71811	12	4038	86.6	1198	10
Aaa88907 Human int	AAA88907	4	4038	86.6	1198	9
Aat85827 Human int	AAT85827	Ν	4009	86.6	1198	80
Aec15897 Human int	AEC15897	14	4006	86.6	1198	7
	ACF87407	13	4006	86.6	1198	თ
Abd20878 Human pul	ABD20878	11	3999	86.6	1198	v
Abz97029 Human nuc	ABZ97029	10	3999	86.6	1198	4
Aaf21335 Human low	AAF21335	ω	3999	86.6	1198	w
Aaa35213 Human ade	AAA35213	ω	3999	86.6	1198	N
a. n	AAT66165	Ν	1383	100.0	1383	
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2331	2331	2331	2331	1389	1995	2382	2382	2355	2355	966	1284	3906	1284	3880	14978	14978	14978	14978	11927	11927	4466	4039	4039	4039	4039	4039
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AEC31479	AEC31477	AEC31483	AEC31481	ADO26893	ADF17840	AAD63744	AAA09050	AAD63743	AAA09049	AAD22979	ADF17834	AAF98394	ADV42774	ABK35718	ABD20881	ABZ97032	AAF21338	AAA35216	AAA90388	AAX77356	ADB47358	ADX97460	ACN41073	ADR24772	ADN04503	ADL82842
Human		Human	Aec31481 Human IL-	Ado26893 cDNA enco	Adf17840 cDNA enco	Aad63744 Human IL-	Aaa09050 IL-13/IL-	Aad63743 Human IL-	Aaa09049 IL-13/IL-	Aad22979 Human sol	Adf17834 Human IL-	Aaf98394 Human cDN	Adv42774 Human psy	Abk35718 cDNA sequ	Abd20881 Human pul	Abz97032 Human nuc	Aaf21338 Human low			Aax77356 Polynucle	Adb47358 Human cDN	Adx97460 Pancreati	Acn41073 Tumour-as	Adr24772 Breast ca	Adn04503 Antipsori	Adl82842 Human PRO

ALIGNMENTS

Human interleukin-12 receptor alpha chain NR4 DNA.

15-JUL-1997

(first entry)

AAT66165;

AAT66165 standard; DNA; 1383 BP.

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23-OCT-1995;
22-DEC-1995;
09-SEP-1996;
                                                                                                                                                     Key
          WPI; 1997-259018/23.
P-PSDB; AAW09822.
                                                                                                                          mať_peptide
                                                                                                                                     sig_peptide
                             Willson T,
                                          (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                               23-OCT-1996;
                                                                                            01-MAY-1997.
                                                                                                        WO9715663-A1
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                  NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine; allergy; asthma; therapy; ss.
                             Nicola NA,
                                                     95AU-00006135.
95AU-00007276.
96AU-00002208.
                                                                               96WO-AU000668
                                                                                                                     /*tag= a
61. .141
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142. .1338
/*tag= c
                                                                                                                                                    Location/Qualifiers 61. .1341
                             Hilton DJ,
                            Metcalf D,
                            Zhang
                             JG;
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DNA encoding animal haemopoietin receptor which interacts with

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Matches 1383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-13 - useful by IgE production.
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TTAACTTCCCGTGTGAAACCTGATCCTCCACATATTAAAAACCTCTCCCTTCCACAATGAT
                                                               GTCCAAATAATGGTCAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCT
                                                                                                                                                                           TATTGGCACAGAAGCCTGGAAAAAATTCAATCAATGTGAAAACATCTTTAGAGAAAGGCCAA
                                                                                                                                                                                                                                  GAAGGTGATCCTGAGTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTAC
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                                                                                                                                                           TATTGGCACAGAAGCCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAA
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antisense oligonucleotide related sequence #2902

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory

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Best Local S
Matches 1248
                                                                                                                                                                                                                                                                                                           transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) end/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressive, antiasthmatic, hypotensive and cytostatic activities, the antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adhesion molecules and their receptors, cytokine and nervous system (CNS) and peripheral nervous and non-nervous system peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
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                                                                                                                                                                                                                                                         mary transplantation rejection, pulmonary infections, bronchitis, cancer. AAF18434 to AAF21543 represent human polynucleotide nts and antisense oligonucleotides used in the exemplification o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIND
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                   CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
                                                         CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTG
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                                                                                           CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTG
invention
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                      GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
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RESULT 4
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                                                                                                                   The invention relates to a novel pharmaceutical composition, which has a CC first active agent comprising an oligonucleotide antisense to the CC initiation codon, coding region, 5 or 3 end genomic flanking regions, CC 5, and 3 intron-exon junctions, or regions within 2-10 nucleotides of CC junctions of genes encoding a polypeptide associated with lung and/or CC nasal airway dysfunction and a second active agent comprising an CC antiinflammatory steroid and ubiquinone. A composition of the invention CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, claimunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also CC for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting lévels CC for reducing sensitivity to adenosine, reducing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or CC lung surfactant in a subject's tissue, or treating bronchoconstriction. CC Note: The sequence data for this patent is not represented in the printed CC specification, but was obtained in electronic format directly from WIPO at first wipo.int/pub/published_pct_sequences
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CC composition of ligonucleotides, effective for alleviating
CC treation adenosine sensitivity, levels of adenosine (A) are respiratory
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (A) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystlc fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted nucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                               This invention
                                                                                                                                                                                                                                                                                              Claim
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                                                           CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA
                                                                                                                                                               GAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA
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reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated
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Sequence 3999 BP; 1127 A; 826 C; 882 G; TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTG CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG Mismatches 0 1164 T; 0 DB <u>+</u> Indels U; 0 Other; 0; 194 254 170 230 0

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The invention relates to a novel method for in vitro detection systemic inflammatory response syndrome (SIRS). The method commodetecting abnormal expression of disease related genes, or their associated peptides. The method of the invention demonstrates
                                                                                                                                                                               02-APR-2003; 2003DE-01015031.
08-AUG-2003; 2003DE-01036511.
02-SEP-2003; 2003DE-01040395.
                                                                                                                                                                                                                                                                                                             Systemic inflammatory response syndrome; SIRS; antibacterial; immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
                                                                         conditions, expression
                                                                                                                                                                                                                                                                                                                                                                    02-JUN-2005
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                                                                        detection of systemic inflammatory response syndrome and ns, for e.g. monitoring progression, comprises detecting a on of disease-related genes.
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                                 ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA
                                                                          GAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA
                                                                                                                    CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
                                                                                                                                                CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCCAAATAATGGT
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 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA
                                                              GAAACCTGATCCTCCACATATTAAAAACCTCTCCCTTCCACAATGATGACCTATATGTGCA
                                                                                                       CAAGGATAATGCAGGAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
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cc may be used for early differential diagnosis, monitoring progression, cc assessing risk, assessing the likely response to treatment and for post concern diagnosis of systemic inflammatory response syndrome, sepsis and cc sepsis-like conditions. The recombinant or synthetic nucleic acid csequences of the invention, or derived proteins or peptides, may be cuseful as calibrants in assays for the specified diseases, for evaluating cuseful as calibrants in assays for the specified diseases, for evaluating cc divity or toxicity in screening for active agents and/or for cc diseases. The current sequence is that of a human SIRS/sepsis diagnostic comarker DNA fragment of the invention. Note: The sequence data for this custom at did not format directly from WIPO at ftp. wipo.int/pub/published cot sequences. Furthermore, a number of arbitrary SEQ ID NO.s are count during indexing due to inconsistencies in application and for format account during indexing due to inconsistencies in application and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial, immunosuppressive and antiinflammatory applications
86.6%; ilarity 99.9%; Conservative
                                                                                                                                                      BP; 1129
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Pred. No. 0;
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GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTTGGCACAGAAG GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG GTCTGCTGTGACTGAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGGTCCCAGTGTAGCACCAATGA TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 0 Mismatches 1; Indels 0 Gaps 434 554 480 494 420 360 300 240 254 180 194 0

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18-MAY-2001; 2001US-0292217P.
20-JUL-2001; 2001US-0306883P.
                                                                                                 20-AUG-2004; 2004US-00922675
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/product= "Interleukin-13 receptor alpha 1 (IL-13RA1)"
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13-AUG-2001;
20-FEB-2002;
06-MAR-2002;
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17-MAY-2002;
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29-AUG-
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2004WO-US016390.
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2003US-00757803.
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                                                                                                                                                                                                Beigelman
                                                                                                                                                                                                         THERAPEUTICS
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New chemically synthesized double stranded siNA molecule that directs cleavage of an Interleukin-13 receptor (IL-13R) RNA via RNA interference, useful in preparing a composition for treating e.g., inflammatory

Page; 127pp; English.

The invention relates to chemically synthesized short interfering nucleic acids (siNAs) which downregulate expression of receptors for interleukin-CC acids (siNAs) which downregulate expression of receptors for interleukin-CC (siny). IL-13 receptor (IL-R) and IL-2 CC receptor gamma (IL-ER)) by RNA interference. The invention also relates to similar siNAs which interfere with the expression of the ligands for CC these receptors, namely IL-13 and IL-4. The siNAs of the invention may or these receptors, namely IL-13 and IL-4. The siNAs of the invention may or comprise ribonucleotides, can contain deoxyribonucleotides, can comprise sense and antisense regions, or alternatively are assembled from the chemically modified and may be double or single stranded. They further comprise sense and antisense oligonucleotide. Specifically, the siNAs include short interfering RNA (siRNA), double-stranded RNA, CC micro-RNA (miRNA) and short hairpin RNA (siRNA), because of the invention also comprising an siNA targeted to micro-RNA (miRNA) and short hairpin RNA (siRNA), see RefSeq accession number CC magnetis to pharmaceutical compositions comprising an siNA targeted to modified. The invention further discloses expression vectors and the stransplant of the invention. The siNAs shown in CC magnetis and siNA of the invention. The siNAs exhibit concreased resistance to nuclease degradation compared to the prior art. The siNAs of the invention and the invention of their can be used to modulate expression of their can be siNAs exhibit and the siNAs of the inventions. They may be used in the createnent of cancers and other proliferative conditions, vital infection, can be used to modulate expression of their can be seases, conditions, vital infection, alternate to conditions, vital infection, the seases, can determine diseases, renal compared to obstructive pulmonary diseases, renal compared to standard diseases, renal compare endocrine diseases, prion diseases and reproduction-related condition. The siNAs may also be used in drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function, and gene mapping (e.g., of single nucleotide polymorphisms). The present sequence represents a corresponding to human IL-13RA1 mRNA, which is specifically claimed a cDNA as a

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This sequence encodes human interleukin-13 (IL-13) alpha receptor. The invention relates to new purified peptides comprising 380 or 427 amino acid sequences, which are receptors for interleukin-13 (IL-13); the 380 and 427 am proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low affinity, but acquires high affinity when associated with the IL-4 receptor. Nucleic acids encoding IL-13R beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta

amino

IL-13R beta

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                                                                                                       New purified human interleukin-13 receptors - and related nucleic useful for diagnosis and treatment of inflammation, allergy, etc.
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CC Capable of binding human interleukin-13 (IL-13) and/or human interleukin-16 (IL-14) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR CC primers (see AAA88908-10) were designed from expressed sequence tags isolated from a database using mouse IL-13 receptor alpha. The primers CC were used to amplify human IL-13 receptor CDNA, from activated tonsilar B CC cell cDNA, The resulting cDNA fragment was used to screen a lambda gt10 CC library of activated tonsilar B cell cDNA and sequencing of the largest CC cDNA insert provided the present sequence. This IL-13 receptor alpha-1 CC cDNA insert provided the present sequence. This IL-13 receptor alpha-1 CC can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells, useful in the treatment of diseases where IgE or Th2 differentiation CC plays a role, e.g. atopy, atopic dermatitis, allergy, thinitis, eczema, asthma or AIDS. Antibodies raised against the pulpaghtide are useful for detecting IL-13 and IL-4 receptor or parts of them which have been shed CC dermatitis, allergies, rhinitis, eczema, asthma, arby, atopic cerythematosus, thyroiditis, diabetes, uveitis, dermatitis, psoriasis, crown's disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome and crown and collegative colitis, Crohn's disease, Sjogren's syndrome and
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                                                                                                                 GAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA
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eczema; asthma; AIDS; gene therapy; gene; ss; interleukin.
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Matches 1248
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06-APR-2000;
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding a polypeptide capable of binding human IL-13 and/or binding human IL-4, useful in medicine, in diagnostics or for producing antibodies.
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AAA35214 standard; DNA; 4039 ВP

(first entry)

Human adenosine receptor related polynucleotide 2nd SEQ ID NO:88

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                                                                                                                                                                                                                                                                                                                                CC oligonuclectide (ON) with low adenosine (up to 15%), which targets conclude condition (on the composition) allergies, and/or CC inflammation. The ON can have antiinflammatory, antiallergic, and/or CC inflammation. The ON can have antiinflammatory, antiallergic, and/or CC inflammation. The ON can have antiinflammatory, antiallergic, and/or CC inflammation, the treatment of diseases associated with inflammation, CC impaired airways, including lung disease and diseases whose secondary CC effects afflict the lungs of a subject. They can be used for treating CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, complete respiration, respiratory distress syndrome, pain, cystic CC impeded respiration, respiratory distress syndrome, pain, cystic CC impeded respiration, respiratory distress syndrome, pain, cystic CC indepeded respiration, respiratory distress syndrome, pain, cystic CC carcinomas, and cancers which may metastasise to the lungs, including CC carcinomas, and cancers which may metastasise to the lungs, including CC carcinomas, and cancers which may metastasise to the lungs, including CC construction of decoxyadenosine which activates adenosine receptors causing CC prometrion, which correspond to SEQ ID NO:11 to AAA35312 represent the CC invention, which correspond to SEQ ID NO:11 to 2815, and then the last 185 content of previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA3992) are specifically claimed ONs from the present invention on the match CC up with their corresponding SEQ ID NO: sequences given in the sequence cC listing from the present corresponding SEQ ID NO: sequences given in the sequence cC listing the corresponding SEQ ID NO: sequences given in the sequence cC listing the corresponding SEQ ID NO: sequences given in the sequence cC listing the corresponding SEQ ID NO: sequences given in the sequence cC listing the corresponding SEQ ID NO: sequences given in the sequence cC listing the corresponding SEQ ID NO: sequences given in the sequence corresponding 
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Matches 1248;
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                                                                                                                                                                                                                                                                               Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
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                                                                                                         CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
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The present invention describes low adenosine (A) content antisens#
CC oligonucleotides and compositions (I) comprising them. In the anti#ense
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with;
CC lung/respiratory disorders and malignancies, such as stimulating and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC chemokines, inding proteins, adenosine receptors, bradykinin receptors, cytokine and
CC chemokines, inding proteins and malignancy associated proteins. The
CC condition specific may be used in this way to treat disorders
CC receptors, binding proteins and malignancy associated proteins. The
CC including respiratory obstruction (especially pulmonary obstruction
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vascocnstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
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AAF21336
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                                                                                                                                                                                                                                                                                                                                                                                                                       Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1999;
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pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
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                                                                                                                                                               ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC
                                                                                                                                                                                                         ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC
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2000US - 0234034P

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CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA

CACAGTAATATGGACATGGAATCCACCCGAGGGGAGCCAGCTCAAATTGTAGTCTATGGTA CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG

CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG

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The present invention describes a method (M1) for screening for an anti-
cone plastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
comprises a sequence (S) selected from 847 sequences (given in ABL61664
comprises a sequence (S) selected from 847 sequences (given in ABL61664
comprises a sequence (S) selected from 847 sequences (given in ABL61664
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comprises a sequence (S) selected from 847 sequencing a product which is
comprises in indicative of anti-neoplastic agent as a result
comprises a sequence (S) selected which respect to the anti-neoplastic agent as a result
comprises of the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
corrective or panoreatic cancer, adenocarcinoma, carcinoma, clear cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
Query Match
Best Local Sim:
Matches 1248;
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29-SEP-2000;

02-OCT-2000;

02-OCT-2000;

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02-OCT-2000;

02-OCT-2000;

03-OCT-2000;

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01-NOV-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for anti-neoplastic agent involves exposing cells to a agent to be tested for anti-neoplastic activity, and determining in expression of a gene of a signature gene set.
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                                                                     Sequence 4039 BP; 1135 A; 839
                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                   Similarity
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Weaver Z;
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2000US-0237173P.

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2000US-0237278P.

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2000US-0237295P.

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2000US-0237425P.

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2000US-0237604P.

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                 Score 1198;
Pred. No. 0;
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   Mismatches
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adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                     WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis; glomerulonephritis; asthma; thrombosi cardiac reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                          2001WO-US030821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocytic cells #1324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombosis;
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity. Claim 1; SEQ ID NO 1324; 114pp; English.

Beazer-Barclay Y,

Weissman

SM,

Yamaga

(GENE-)

GENE LOGIC INC

CC (WAA), by detecting the level of expression of gene(s) (GS), identified by CC (C), and comparing the expression level to an expression of gene(s) (GS), and comparing the CC expression level to an expression level in an unactivated GC, where CC differential expression of GS is indicative of GCA. Also included are CC tasue, an alteract compable of modulating GCA or an inflammation (especially chronic) in a CC tissue, an altergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease using the gene expression of the gene in inflammation (especially chronic) in a CC tissue, an altergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating CC (MS) an inflammation (especially chronic) in a CC inflammatory disease, by contacting a tissue having Gis in the tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue; Al is useful for modulating GA; MJ is useful for screening an agent capable of modulating GA preferably in an CC inflammation in a tissue; Al is useful for detecting GA; MJ is useful for screening an inflammation with an altergic response in a subject, capable of modulating GA preferably in an inflammation with an inflammation with an altergic response in a subject, capable of modulating GA preferably in an inflammation with an altergic response in a subject, capable of modulating GA; MJ is useful for detecting an inflammation with an altergic response in a subject, capable of modulating GA; MJ is useful consists, remained by a contacting GA; MJ is useful for careful and the consisting of the subject, capable of modulating GA; MJ is useful for treating one of the above of the subject in the present sequence represents a gene differentially capable of the consisting of the above of the consisting for the su invention relates to by detecting the level of detecting (M1) granulocyte expression of gene(s) C) activation (Gs) identified γď

BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

RESULT 15
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ID ABK84
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AC ABK84
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AC ABK84
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ABK84753

standard;

cDNA;

4039

14-AUG-2002

(first entry)

Query Match Best Local Similarity 86.6**%**; 99.9**%**; Score 1198; Pred. No. 0; DВ 9 Length 4039;

70 AG

Matches	1248; Conservative 0; Mismatches 1; Indels 0; Gapt 0;
; \$	35 CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTG 19
, 6	ZI UGUGUTAAAACICAGCCAGCTIGIGACAAAITIGAGTGICTUIGITIGAAAACCTUIG I
Db 2y	195 CACAGTAATATGGACATGGAATCCACCGCAGGGACCAGCTCAAATTGTAGTCTATGGTA 254 181 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 240 181 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 240
Ωy	TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGGAAACTCGTCGTTG
ОЪ	41 TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTTCGGAAACTCGTCGTTCAAT 3
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ş	95 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG 55
Db	81 GCTCCCTGGAAGGAATACCA
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do	41 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC
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O _V	75 CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT 73
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γ ₂ γ	735 GAAACCTGATCCTCCACATATTAAAAACCTCTCCTCCACAATGATGACCTATATGTGCA 794
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ργ	5 CAGCCAAACTGAGACACATAATGTT
Ъ	1 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA 9
ΥC	915 ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 974
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Dy J	5 AACCATGTTACTCATTGTT
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REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS SOURCE RESULT 1
AR691934
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DEFINITION
ACCESSION S 밁 Ś 밁 8 밁 S ORIGIN FEATURES Matches 1383; Query Match Best Local Similarity ORGANISM source 181 181 121 121 61 61 1 (bases 1 to 1383)
Willson,T., Nicola,N.A., Hilton,D.J., Metcal
Haemopoietin receptor and genetic sequences
Patent: US 6911530-A 3 28-JUN-2005; Unknown. AR691934 Sequence 3 from AR691934 Unclassified. Amrad Operations, Unknown. AR691934.1 GTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCCACCCGAGGGAGCCAGCTCAAAT GGCGGGGGCGGGCCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCT GAGTCTAACACGGACCAAGGAGTTTAACACGTGCGGCCGGGTTCCGAGGCGAGAGGCTGC GTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAAT GGCGGGGGGGGGGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCT GAGTCTAACACGGACCAAGGAGTTTAACACGTGCGGCCGGGTTCCGAGGCGAGAGGCTGC Conservative /organism="unknown" /mol_type="genomic DNA" Location/Qualifiers 100.0%; 1383 bp / patent US 6911530. Pty., Ltd.; ٥, Score 1383; Pred. No. 0; Mismatches Richmond; DNA DB Metcalf, D. 0; ر. د Length 1383; Indels linear encoding and PAT <u>.</u>; 13-SEP-2005 Gaps à ົດ 120 180 180 60 240 120 60 0

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Medicine, Maidashi, Fukuoka 812-82, Japan
Sequence update by submitter
On Sep 13, 1999 this sequence version replaced
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-JUN-1999) Biochemistry, Kyus Medicine, Maidashi, Fukuoka 812-82, Japan Sequence update by submitter 3 (Dases 1 to 1708) Wada, M., Hisano, T. and Kuwano, M. Direct Submission
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                                                     CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
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                                  CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
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LCTYLWWWNEDEGASSNCSLWYESHFGDKQDKLTAPETRSIEVPLNERICLQVCSQC
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YYWHRSLEKIHQCENIFREGQYPGCSFDLTKVKDSFEQHSVQIMVKDNAGKIKPSFN
LVPLTSRVKDDPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNUSQTETHNVFY
VQEAKCENPEFERNVENTSCFMVPGULPDTLATVVRIKVKTUKLCYEDDKHKNSNWSQBS
VQEAKCENPEFERNVENTSCFMVPGULPDTLATVVRIKVKTUKLCYEDDKHKNSNWSQBS
SIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYKKRLKIIIFPPIPDPGKIFKEMPGDQ
SIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYKKRLKIIIFPPIPDPGKIFKEMPGDQ
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/product="interleukin-13 receptor"
/protein_id="AAD00510.3"
/db_xref="GI:5870851"
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/NOT TYPE="MRNA" /Ab vyof="taxon.ofof"	1335 TCAGTGATGAGATAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1383	0
	1258 GAAGCAAACCAAGGAAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC 1317	Db
	1275	ð
Clone distribution: MGC clone distribution information can be found	1198 AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA 1	문
Tsurgeon, C., Vot. Sol., K., Wetherby, K.D., Wiggins, L.,		0
Hansen, N., Ho.SL., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Hansen, N., Ho.SL., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., Manner, J. T., Masseri, B., Mastrian, B. T., McCloskey, J. C., Manner, J. T., Masseri, B., Mastrian, B. T., McCloskey, J. C., Manner, J. T., Masseri, B., Mastrian, B. T., McCloskey, J. C., Manner, J. T., Masseri, B., Mastrian, B. D., McCloskey, J. C., Manner, J. T., McCloskey, J. C., Mastrian, B. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McCloskey, J. C., Manner, J. T., McCloskey, J. C., McClosk	1155 CCTAAAAAGCCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTTAA 1214	음 성
Blakesley, Nyere, N., Beunstrour Stetzberg, S.H., Benjamin, P., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich N.I. Granite S. Ghan Y. Gunta J. Harbichi D.	1078	망
Web site: http://www.nisc.nih.gov/ Contact: nisc mgconhgri.nih.gov/ Akhter N nisc mgconhgri.nih.gov/	1095	Ś
Sequencing Center (NISC), Gaithersburg, Maryland;	1018 CTGGAGTAATTGGAGCCAAGAAATGAGTAATAGGTAAGAAGCGCAATTCCACACTCTACAT	Db
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural	1035 CTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT 1	ρ
Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory	975 TITGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACT 1034 	유왕
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT On Dec 9, 2003 this sequence version replaced gi:14602931.	898	рb
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	915	Ş
JOURNAL Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer	838 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA	망
AUTHORS Director MGC Project.	855 CAGCCAAACTGAGACATAATGTTTTCTACGTCCAAGAGGCTAAAATGTGAGAATCCAGA	5
	/ //95 AIGGGAGAATICCACAGAATITTATTAGCAGATGCTATTTATGAAGTAGAAGTCAATAA 854 	문 원
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	718 GAAARCIGATCCICCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA	? 5
Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. CONSRTM Mammalian Gene Collection Program Team	733 GAMARICEIGATECTICCACATATTAAAARCICTICCTITCCACAATGATGACCTATATGTGCA	; 5
Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,	658 CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT	2 5
Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,	675 CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT	;
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,	598	밁
Scheetz is, biowisserin is, toshiyuki S, tarninci k, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ. Bosak SA. McEwan PJ. McKernan KJ. Walek JA. Gunaratne PH.	ď	Ş
GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,	538	Дb
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,	/ 555 CCTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC 614	Ş
REFERENCE 1 (bases 1 to 2139) AUTHORS Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,	478 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTATTATTGGCACAGAAG 537	Db
	495 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG	γQ
1 Homo sapi Eukaryota	3 418 GTCTGCTGTGACCTCAAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG 477	망
MGC.	435	ð
MGC:15228 IMAGE:4300487), complete cds. BC009960 BC009960.2 GI:39644647	Db 358 GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCAGAAGGTGATCCTGA 434 Db 358 GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA 417	
Homo Homo	270 AVANDIACCCIGANIGAGAGGAITIGICIGCANGIGAGGICCCAGIGIAGCACCAAIGA	
	315 AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA	} &
Db 1318 TCAGTGATGGAGATAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1366		г

/mol_type="mRNA" /db_xref="taxon:9606" organism="Homo sapiens'

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Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Sichards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz JJ, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse CDNA secuences
                              ab site: http://www.nisc.nih.gov/
ntact: nisc_mgc@nhgri.nih.gov/
ntact: nisc_mgc@nhgri.nih.gov

chter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

kakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

letrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

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lamsen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

sunsen,N., Masielilo,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,

Dowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

sungen,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

walker,M.A., Wetherby,K.D., Wiggins,L.,
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NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
A Sequencing by: National Institutes of Health Intramural
quencing Center (NISC),
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ssue Procurement: ATCC
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Dec 9, 2003 this sequence version replaced gi:14602931.
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bmitted (02-JUL-2001) National Institutes of Health, Mammalian collection (MGC), Cancer Genomics Office, National Cancer of the State of the Stat
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/protein_id="AAH09960.1"
/db_xref="GI:14602932"
/db_xref="GeneID:3597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xre1="GELICAL_
/db_xref="MIM:300119"
1314
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/tissue_type="Pancreas, epithelic/
clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"
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/db_xref="GeneID:3597"
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99.9%;
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Pred. No. 0;
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Strauberg, R. L., Feingold, E.A., Grouse, L. H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K. H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsteh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens interleukin 13 receptor, alpha MGC:23204 IMAGE:4868206), complete cds. BC015768 BC015768.1 GI:16041774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Query Match
Best Local Similarity
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skaløka, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Email: cc
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                           /product="interleukin 13 receptor, alpha 1, precursor"
/protein id="AAH15768.1"
/db_xref="GI:16041775"
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YYMHRSLEK.HQCENLTREGQYFGCSFDLTKVKDSSFEGLFYSEVENNSQFEIKPSFN
IVPLTSRYKEDPPHIKMLSFHADDLYVYMENDONISRCLFYSEVENNSQFEIKPSFV
VQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLMSNMSQEM
SIGKKRNSTLYITMLLIVPUTVAGAIIVILLLKKRLKIIIFPPIPDPGKIPKEMFGDQ
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                                                                                                 NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Colon, ad
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/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonyms: IL-13Ra,
/db_xref="GeneID:3597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Vector:
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="IL13RA1"
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     86.6%;
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  Score 1198;
Pred. No. 0;
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  CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTTAA
                                CCTAAAAAGGCTCAAGATTATTATATTCCCCTCCAATTCCTGATCCTTGGCAAGATTTTTAA
                                                                                                                        AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA
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                                                                                            AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA
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1214 1144 1094 1024 1034 964 974 904 914 844 854 794

724 734 664 674

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544 554 484 494 424

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244 254 184 194

y Match Local Similarity 99 hes 1248; Conservativ 135 CGCGCCTACGGAAA 111 CGCGCCTACGGAAA	// Sele="Lil Skal" // Codon start=1 // Codon start=1 // Codon start=1 // Product="Ill3 recepto: // Protein id="CAA70508 // Protein id="CAA70508 // Drotein id="CAA70508 // Drotein id="CAE70508" // CCTVIWTWNPPEGASSNCSLWY STNESERSILVENCSISPEGGY STNESERSILVENCISPEGGY IVPLTSRVXPDPHIKNISFHNI VQEAKCENPEFERNVENTSCFM SIGKKRNSTLYITMLLIVFVIU\/ NDDTLHWKXVDIYEKQTKEETD SONTAIN JOHN SIGNAI" // Gene="Ill3RA1"	/mol_type="manka" /mol_type="manka" /db_xref="taxon:9606" /db_xref="taxon:9606" 1.	-1996) D. Capu x, FRANCE /Qualifiers	SEDF	i Chain; IL13R piens (human) piens (human) piens piens piens (a; Butheria; lae; Homo.	S A1 HSIL13RA1 ION H.sapiens ON Y09328	Qy 1215 AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA
Qy .6%; Score 1198; DB 5; Length 3999; bb.9%; Pred. No. 0; c 0; Mismatches 1; Indels 0; Gaps 0; CTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194	/ Goding start=1 // Coddon start=1 // Coddon start=1 // product="II13 receptor alpha-1 chain" // product="GA7/0508.1" // protein_id="CAA/0508.1" // protein_id="CAA/0508.1" // protein_id="CAA/0508.1" // db_xref="GO1:188508" // db_xref="GO1:1885	Qy Db	, SANOFI Recherche, BP 137, F- Qy Db	1 chain and reconstitution with Db 5-4/IL-13 receptor complex Qy	<pre>3 receptor. tebrata; Euteleostomi; ates; Catarrhini; , Caput,D., Vita,N. and</pre>	mRNA linear PRI 26-FEB-1997 Qy alpha-1 chain.	GACATCTATGA 1274
1155 CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGGATCCTGGCAAGATTTTTAA 1214	915 ATTTGAGAGAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 915 ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 915 ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 975 TTTGAACACAGTCAGAATAAGAGTCAAAAACAAATAAGTTATGCTATGAGAGAGA	771 ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAATCCAGA 9 855 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA 9 867 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA 9	735 711	515 CHARGACCARAGIGANGALICAGILIGANCARACACAGIGCONTALIAMING 671 CHARLAMANGAGIGANGAGIGAGAGAGAGAGAGAGAGAGAGAGAGAG	495 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTACTATTGGCACAGAAG	35 GACTGAGAGCCTACCATTITEGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA 351 GAGTGAGAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA 35 GTCTGCTGTGACTGAACTTCAATGCATTTTGGCACAACCTGAGCTACATGAAGTGTTTCTTTG	195 171 255 231 315 291

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Patent: WO 9720926-A 3 12-JUN-1997;
SANOFI SA (FR)
Other publication AU 7576096 199706
Other publication FR 2742156 199706
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                          CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGT
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Bonnefoy, J. Y. and Gauchat, J. F.
Substances and their uses
Patent: US 6743604-A 8 01-JUN-2004;
Smithkline Beecham Corporation; Philadelphia,
                                                                                                                                                                            Unknown.
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AL Patent: EP 147. Hinzmann, Bernd (DE); Dahl, Edd (DE)	555 CCTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC 614 	Qy dd
REFERENCE 1 AUTHORS ROSenthal, A. D., Pilarsky, C., I Lichtner, R., Staub, E., Roepcke Lichtner, B., Staub, E., Roepcke TITLE Human nucleic acid semmences e	495 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCCTACTATTGGCACAGAAG 554 	D Qy
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hal, Andre (DE); Pilarsky, Christian
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                                                                Homo
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                                       Hominidae;
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Patent: WO 0194629-A 6046 13-
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Location/Qualifiers
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                                                                     CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Gene expression profiles in liver cancer
Patent: WO 0229103-A 3859 11-APR-2002;
GENE LOGIC INC (US)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
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/note="EMBL/GenBank Accession
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A novel 4 kb IL-13Ra mRNA expressed in human B, T and endothelia cells, encoding for an alternate type two IL-4/IL-13R
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Submitted (20-UAN-1997) J-F.M. Gauchat, Geneva Biomedical Research Institute, Immunology, Glaxo Research And Development, 14 Ch Des Aulx, Plan-Les-Ouates, CH1228, SWITZERLAND
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2 (bases 1 to 4039)
Gauchat, J.F.M.
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Mammalia; Eutheria;
GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG
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VQBAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLMSNMSQEM

SIGKKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIPDFKIFKEMFGDQ

NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="3.1"
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/clone_lib="Lambda gt10"
/dev_stage="adult"
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Renner W.A., Orberger, G.H., Koller, D. and Bailey, J.E.

Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property

Patent: US 6524792-A 5 25-FEB-2003;
Cytos Biotechnology; Zurich-Schlieren;
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             ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC
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Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1284)
Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and LaBaer,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY892945 1284 bp mRNA linear SYN 29-MAR-20 Synthetic construct Homo sapiens clone FLH141766.01L interleukin receptor alpha 1 (IL13RA1) mRNA, partial cds.
                                                                                                                                                                                                                  reading frame. Easequence-verified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and LaBaer,J.
Cloning of human full-length CDS in Creator (TM) recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                             /organism="synthetic construct"
/mol type="mRNA"
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LCTVINTWNPPEGASSNCSLWYESHFGDKQDKKLAPETTRSIEVPLNRERICLCYVGSQC
STNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSWLPGRNT9PDTNYTC
YYWHRSLEKIHQCENIFREGQYFGCSFDLTKYKDSSFEGHSVQLIWYKDNAGKIKPSFN
IVPLTSRVKEDDPHIKNLSFHNDDLYVQMENPQNFISRCLFYEVEVNNSQTETHNVFY
VQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLMSNMSQEM
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NDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQL"
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/protein_id="AAX29862.
/db_xref="GI:60654343"
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/codon_start=1
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                                       Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, bepartment of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp, UKL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930, Fax:81-438-52-3931)

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UKL: http://protein.gsc.riken.go.jp/.
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2 (bases 1 to 3960)
Totoki, Y., Toyoda, A., Takeda, T., Sa
Ohara, O., Nagase, T. and F. Kikuno, R.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB209849
                                                                                                                                                                                                                                                Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                              None Title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGGCCAAGATTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAGTAATTGGAGCCAAGAAATGAGTAATAGGTAAGAAGCGCAATTCCACACTCTACAT
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                                                                                                                                                                                                                                              Submission
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/organism="Homo sapiens"
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:62089283
                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                             Sakaki,
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ORIGIN
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Matches 1247
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                                                             CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
                                                                                                           CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACACAGTGTCCAAATAATGGT
                                                                                                                                                                                                                                                                               GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG
                                                                                                                                                                                                                                                                                                                                                          GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG
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GAAACCTGATCCTCCACATATTAAAAACCTCTCCCTCCACAATGATGACCTATATGTGCA
                                                                                                                                                                                    CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC
                                                                                                                                                                                                                                                                                                                                   GTCTGCTGTGACTGAGCTTCAATGCATTTTGCACAACCTGAGCTACATGAAGTGTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /inference="non-experimental evidence, no addition details recorded"
                                                                                                                                                                                                                                                          /protein_id="BAD93086.1"
/db_xref="G1:62089284"
/translation="EWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENL
/translation="EWPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENL
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/translation="EWPARLCGLWALLCAGGGGGGGAAPTETQPPVLNSRICLQVGSQCS
TNESEKPSILVEKCISPPEGDFSAVTELQCILHNLSYMKCSWLPGRWTSPDTNYTLY
YWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNI
VPLTSRVKPPDFPHIKNLSFHNDDLYVQMENTISRCCLFYEEVENNNSQTETHAVFYV
QEAKCENPEFRUNDTSCFMVFGVLPDTLMTVRIRKTKLCYEDDKLMSNMSQEMS
IGKKRNSTLYITMLLIVPVIVAGAIIVLLYLKRLKIIIFPPIPDPGKIFKEMFGDQN
DDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variant"
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<1. .1282
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/db_xref="taxon:9606"
/clone="ef01196"
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/codon_start=2
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                                                                                                                                                                                                                                                                                                                           AX099392
Sequence
AX099392
                                                                                                                      Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L., Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Assecreted proteins and polynucleotides encoding them Patent: WO 0119988-A 32 22-MAR-2001;
Genetics Institute, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                    Homo
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                                                                 /mol_type="unassigned
/db_xref="taxon:9606"
                                                                                               organism="Homo sapiens"
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Butheria; Euarchontoglires; Primates; Catarrhini;
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             99.8%;
                Score
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Agostino,M.J.
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.283	1224 TGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAAC 1	
080	1021 GCTCAAGATTATTATTATTATCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTT 1	
.02	104 ACTCATTGTTCCAGTCGATGCAGTGCAATCATAGTACTCCTGCTTTACCTAAAAAG	
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983	924 AAATGIGGAGAAIACAICITGTTICATGGICCCTGGIGTTCTTCCTGAIACTTIGAACAC 9 	
)23 780	TGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGA	
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383 240	CCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAA	
323	TTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACC	
263	Aaattgtagtctatggtatttagtca 	
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1344 GAGATAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1383
1141 CAAGGAAGCAACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATG 1200
1284 CAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAAACCTGAAGAAAGCCTCTCAGTGATG 1343
1081 TGGAGACCAGAATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAAC 1140

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ALIGNMENTS

REFERENCE AUTHORS REFERENCE AUTHORS VERSION KEYWORDS SOURCE RESULT 1 CR603161 LOCUS ORIGIN FEATURES COMMENT ACCESSION DEFINITION TITLE JOURNAL TITLE JOURNAL ORGANISM REMARK source 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens CR603161.1 GI:50483968 HTC; CNSLT_cDNA. full-length cDNA clone CSODIO01YN10 of Placenta Cot of Homo sapiens (human). Genoscope Hominidae; CR603161 CR603161 Web : www.genoscope.cns.fr) (bases 1 to 1756) (bases 1 to 1756) iday Avenue sapiens (human) /organism="Homo sapiens" /mol type="mRNA" /mol type="mRNA" /db_xref="taxon:9606" /clone="CSUDI001YN10" /tissue_type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6" Location/Qualifiers Homo. 1756 bp mRNA linear HTC 21-JUL-2004 25-normalized

Query Match

76.9%;

Score 1063;

DB 6;

Length 1756;

δδ	1155 CCTAAAAAGGCTCAAGATTATTATATTCCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA 1214	8
da Qy	1095 AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA 1154	B 8
dd	1035 CIGGAGTAATIGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACCTCTACAT 1094	d dd
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OV В	858 ATTTGAAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 917 975 TTTGAACACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACT 1034	Q B
ρ	ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC	Ş.
Query Best Match	855 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA 914 	og Qy
ORIGIN	795 ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA 854 	d da
	735 GAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA 794	₽ &
	675 CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT 734 [g Q
FEATURE	615 CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGT 674	망양
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	495 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG 554	dg VQ
JOURN	435 GTCTGCTGTGACTGAACTTCAATGCATTTGGCACACCTGAGCTACATGAAGTGTTCTTG 494	dg VQ
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SOURCE	315 AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA 374 	g &
ACCESSI VERSION KEYWORD	255 TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT 314	B &
RESULT AL54333 LOCUS DEFINIT	195 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 254 	δ Q
αα	78 CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 137	р 5
Qy	1113; Conservative 0; Mismatches 1; Indels 0; Gaps	Mat
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
11048.f
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Similarity 99.9%;
GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA
                                                                                   AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGGTCCCAGTGTAGCACCAATGA
                                                                                                                                                                                        TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/db_xref="taxon:9606"
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TITLE
JOURNAL
COMMENT
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VERSION
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    source
          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12279 row: p column: 21
High quality sequence stop: 719.
Location/Qualifiers
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1 (bases 1 to 951)

NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                           BM905033 951
AGENCOURT_6699542 NIH_MGC_72
5', mRNA sequence.
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EST.
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                                                               GTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTGGAGAATACATCTTG
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/organism="Homo sapiens"
/mol_Type="mRNA,"
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/tissue_type="melanotic melanoma"
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/note="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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GTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGAAATGTGGAGAATACATCTTG TTTGAACAACACACTGTCCAAATAATGGTCAAGGATAATGCAGGAAAAATTAAACCATCC TTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAAGTGAAGGATTCCAGT AACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAATTCATCAATGTGAAAACATC AAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCCCTGAATGAGAGGATTTGTCTG TGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTAC TGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTAC TGCATCTCACCCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAACTTCAATGCATTTGG CAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAAGCCCTAGCATTTTGGTTGAAAAA AATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAG AACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAAATTCATCAATGTGAAAAACATC CAAGTGGGGTCCCAGTGTAGCACCAATGAGAGTGAGAAGCCTAGCATTTTGGTTGAAAAA **AATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAG** TGCATCTCACCCCAGAAGGTGATCCTGAGTCTGCTGTGACTGAGCTTCAATGCATTTGG Conservative 52.6%; Score 728; DB Pred. No. 0; 0; Mismatches ٥, DB u •• 1; Length Indels 0 Gaps 612 885 672 825 765 552 705 492 645 432 585 372 525 312 465 252 405 192 345 132 285 72 225 0

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Submitted (05-MAY-2005) Celera Genomics, 45 West Gude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T. Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. A Scan for Positively Selected Genes in the Genomes of Humans a Chimpanzees
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DQ034842.1 GI:66886051
GSS.
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This sequence was made by
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                            GGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTTGGAAAAAA
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                     TTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGA
                                                                                                                                            CTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGAA
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(bases 1 to 866)
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/locus_tag="HC4262"
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99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CK000442 842 bp mRNA
AGENCOURT 16363365 NIH MGC 221 Homo sapiens
IMAGE 30708826 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM1075 row: k column: 11
High quality sequence stop: 681.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol type="make"
/mol type="make"
/db_xref="taxon:9606"
/clone="IMAGE:30708826"
/lab_host="PlAIOB TonA"
/clone_lib="NIH_MGC_221"
/clone_lib="NIH_MGC_221"
/note="forgan: mixed; Vector: pYX-Asc; Site_1: EcoRI;
/cloned_Denatured_RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according tomaNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
4-5Kb. Adaptors 5'(AATTCGGCACGAGG)3' and 5'd
(CCTCCTGCGCG]3'. 3' Linker sequence - GCGGCCGCTGAGAGGCC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
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              Hominidae; Homo.

1 (bases 1 to 799)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                                                                                  AGENCOURT 13666655 NIH MGC_184 Homo IMAGE:30353391 5', mRNA sequence. CB956372 CB956372.1 GI:30212489 EST.
                                                                                                                  Homo sapiens
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                     Homo
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Strausberg,
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            ACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATG 797
                                                         GGATAATGCAGGAAAAATTTAAACCATCCTTCAATATAGTGCCTTTTAACTTCCCGTGTGAA
                                                                                                                   TGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAA
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/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
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EST.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                         GCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAAT
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Location/Qualifiers
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/rote="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, MTERT-HME1, LNCaP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:6721041"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 633)
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CA391344
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CS14a05.yl Human Retinal pigment
(Un-normalized, unamplified): cs
                                                                                                                                                                                                                                                             National Eye Institute 6/331, NIH, Bethesda, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA391344.1
                                                                                                                                                                                     Email: graeme@helix.nih.gov
Plate: 14 row: a column:
                                                                                                                                                                                                                         Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                  Section on Molecular Structure
                                                                                                                                                                                                                                                                                                                     Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                      12107410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                 primer: M13RP1 reverse primer
Location/Qualifiers
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs14a05"
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                                                                                                                                                                                                                                                                                                    and Function
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                                                                                                                                                                                                                                                                                          GGATAATGCAGGAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAA
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/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally clonded cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen CORD), essentially, following the protocols of the SuperScript Plasmid System (Invitrogen Corp., chtp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                      BRACE3 Homo
    GI:78564889
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99.8%;
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clone
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                                                                 EST 01-NOV-2005
9 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
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1 (bases 1 to 580)

Kimura, K., Wakamatsu, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Takao Isogai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                              GAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAAC 1097
                                                                                                                GAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTG 103:
                                                                                                                                                                          CCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATT
                                                                                                                                                                                                                                                                                                                                                                                GGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAG
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    GAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAAC
                                                                                      GAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTG
                                                                                                                                                                                                                                                                   CCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATT
                                                                                                                                                                                                                                                                                                                                                         GGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 577; DB 9; Lot 100.0%; Pred. No. 3.1e-302; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cerebellum"
/clone_lib="BRACE3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRACE3014879"
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Genome Res. 16 (1), 55
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
                                                                               755
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                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
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2-6-7 Kazusa-Kamatari, Kisarazu,
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1 (bases 1 to 573)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                              TTAAAAAACCTCTCCCTTCCACAATGATGACCTATATGTGCAATGGGAGAATCCACAGAATT
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/tissue_type="thymus"
/clone_Tib="THYMU3"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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DA757245
                                                                                        Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
                                                                                                                                    FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, K
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1 (bases 1 to 567)
                                                                                                                                                                                        Contact: Takao Isogai
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes Genome Res. 16 (1), 55-65 (2006) NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); CDNA library construction: Helix Research Institute (HRI); 5' end one pass sequencing; HRI, Research Association for Biotechnology (RAB) and Biotechnology (Center, National Institute of Technology and Evaluation; 3'-end of the Context of Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; bp mRNA linear EST (cDNA clone NT2RP8004310 5'; Chiba, 292-0818, Japan EST 03-DEC-2005 Wagatsuma, M., one

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1 (bases 1 to 570)

Kimura, K., Wakamatsu, A.,
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                              Homo sapiens
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                                                                                                                                     NT2RI2 Homo sapiens
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/note="Vector: pME18SFL3; mRNA from NT2 neuronal
cells after 5-weeks retinoic acid (RA) induction"
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/cell_line="NT2"
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/clone="NT2RP8004310"
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/db_xref="taxon:9606"
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                                                                                                      GI:82349574
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                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 8.8e-297;
Suzuki,Y.,
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cDNA clone
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Ota,T.,
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NT2RI2011802
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829 CTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTACGTC
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Promoters of Human Genes
16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com

REMail: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing: RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takao Isogai
FLJ Project (HRI Team)
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                                                                                                                                                                                                        GGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGGCTCAAGATTATTATATATTCCCTCCA 1188
                                                                                                                                                                                                                                                                                                                                AAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCA 1128
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AAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGCCAAGAAATGAGTATAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGCCAAGAAATGAGTATAGGT 1068
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                                                                                      ATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACTCTG 1248
                                                                                                                                                                                                                                                                                           AAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCA
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81-438-52-3986
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/cell line="NTZ"
/cell line="NTZ"
/clone lib="NTZRI2"
/clone lib="NTZRI2"
/note="Vector: pME188FL3; majorly NT2 neuron; mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 3.1e-290;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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1 (bases 1 to 552)

1 (bases 1 to 552)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishidashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative
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DA992396.1
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DA992396
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2-6-7 Kazusa-Kamatari, Kisarazu,
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Genome Res. 16 (1), 55-65 (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                          GGCCAATACTTTGGTTCCTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAA
                                                                                                                                                                              CTCTACTATTGGCACAGAAGCCTGGAAAAAATTCATCAATGTGAAAAACATCTTTAGAGAA
                                                                                                                                                      CTCTACTATTGGCACAGAAGCCTGGAAAAATTCATCATGTGAAAACATCTTTAGAGAA
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SYNOV4 Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                            /clone_lib="SYNOV4"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                              /tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                  /mo1_type="mRNA"
/db_xref="taxon:9606"
/clone="SYNOV4004609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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                                                                                                                                                                                                                                                            39.9%;
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                                                                                                                                                                                                                                                              Score 552;
Pred. No.
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                                                                                                                                                                                                                                                                                    DB 9;
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clone SYNOV4004609
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DA990183
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DA990183
                                                                                                        Email: tlj-cana@nirty.com

NEDO human cDNA project (New Energy and Industrial Technology

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Research Association for Biotechnology and Evaluation; 3'-end
                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 543)

1 (bases 1 to 543)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, I. Murakawa, K., Ishidashi, T., Takahashi-Pujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, Intentification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                           Helix Research Institute
2-6-7 Kazusa-Kamatari, K
                                                                                                                                                                                                                Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                            FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                              Promoters of Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                      Fax: 81-438-52-3986
                                                                                                                                                                                                                                                              Tel: 81-438-52-3975
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  /organism="Homo sapiens"
/mol_type="mRNA"
                                                              Location/Qualifiers
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Homo sapiens cDNA clone SYNOV4001683
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H., Wagatsuma,M.,
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                                                  Hominidae; Homo.

1 (bases 1 to 541)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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                                                                                                                                                                              CB161269
CB161269.1 GI:28147395
EST.
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21C Frontier Korean
Unpublished (2002)
Contact: Kim YS
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/clone_lib="SYNOV4"
/note="Vector: pME18SFL3"
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/clone="SYNOV4001683"
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Pred. No. 1.1e-283;
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Plate: 20 row: D column: 03
High quality sequence stop: 541.
Location/Qualifiers
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Site 2: Not!, The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
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INFORMATION FOR SEQ ID NO: 2902:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO
US-09-543-679A-2902
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US-09-543-679A-2902
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Patent No. 7034007
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSIN
                                                                                                                                         Query Match
Best Local Similarity
Matches 1248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/ACENT INFORMATION:
NAME: AMZEJ, VLYJana
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381
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CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS
STREET: 7 Clarke Drive
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 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
                  CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
                                                                     CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
                                                                                          CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
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STATE: NJ
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                                                                                                                                             Conservative
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                                                                                                                                                            86.6%;
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ON: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
ON COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
                                                                                                                                         0;
                                                                                                                                         Score 1198; D)
Pred. No. 0;
0; Mismatches
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TCAGTGATGGAGATAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1383
                                                                                                                                                                                                                                             CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT 734
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                                            GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
                                                                                                                                               AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA
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US-08-969-125-8
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; SEQUENCE DESCRIPTION: SEQ US-08-969-125-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/969,125B
APPLICATION NUMBER: US/08/969,125B
APPLICATION NUMBER: G143871-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, WARY J.
REGISTRATION NUMBER: 130-179
REGISTRATION UNMBER: 1430-179
REGISTRATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4000
TELEPACE (DOCKET NUMBER: 150-179
TELECOMMUNICATION UNFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4038 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08969125B Patent No. 6143871 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BONNEFOY, JEAN-YVES
315 AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A.
                                                                          TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTTCAAT
                                                                                                                                     CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
                                                                                                                                                             CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA
                                                                                                                                                                                                                    CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
                                                                                                                                                                                                                                               CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
                                                      TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                         86.6%;
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Pred. No. 0;
0; Mismatches
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RESULT 4
US-09-545-002-8
     Sequence 8, Application Patent No. 6743604
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 12-No. 6743504-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
MOLECULE TYPE: I
FRAGMENT TYPE:
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APPLICATION NUMBER: US/09/545,002
FILING DATE: 12-No. 6743604-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 43..1323
SEQUENCE DESCRIPTION: SEQ
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: NIXON & VANDERHYE
STREET: 1100 NORTH GLEBE ROAD
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
------ Datentin Release #1.0, Version
GTCTGCTGTGACTGAACTTCAATGCATTTGGCACCACCTGAGCTACATGAAGTGTTCTTG
                                                         GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA
                                                                              GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA
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STRANDEDNESS: single
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STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                              AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCCAGTGTAGCACCAATGA
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Pred. No. 0;
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RESULT 5
US-09-949-016-223
; Sequence 223, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 135 CGCGCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194	; SOFTWARE: PATENTIN Ver. 2.1 ; SEQ ID NO 3856 ; LENGTH: 4039 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; OTHER INFORMATION: Genbank Accession No. 6974667 Y10659 US-09-880-107-3856		ince 385 it No. 6 to No. 7 to	Qy 1335 TCAGTGATGAGATAATTTATTTTTACCTTCACTGTGACCATGAGAAGA 1383	Qy 1215 AGAANTCTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA 1274	Db 1081 AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGTGCAATCATAGTACTCCTGCTTTA 1140 Qy 1155 CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGGAAGATTTTTÄA 1214	1035 CTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT	Db 901 ATTTGAAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCCTTGATAC 960 975 TTTGAACACAGTCAGAATAAGAGTCAAAAACAAATAAGTTATGCTATGAGGATGACAAACT 1034
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S-09-543-0....
Sequence 2903, Applicate.
General Information:
APPLICANT: NYCE, Jonathan W.
APPLICANT: NYCE, Jonathan W.
COMPOSITIONS KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,
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US-09-543-679A-2903
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US-09-543-679A-2903
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Best Local Similarity
Matches 1248; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 4039 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: 60/127,958
APPLICATION NUMBER: 60/127,958
PILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-006
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: CD-R
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CITY: Cranbury
STATE: NJ
COUNTRY: USA
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                                                         GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA
                                                                                                                      AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA
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     GTCTGCTGTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG
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; Sequence 5, Application US/09193707
; Patent No. 6524792
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
                                                                                                                  RESULT 8
US-09-193-707-5
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; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES;
TITLE OF INVENTION: A PREDETERMINED PROPERTY
FILE REFERENCE: 8358-0005-999
; CURRENT APPLICATION NUMBER: US/09/193,707
; CURRENT FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; SEQ ID NO 5
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; TYPE: DNA
; ORGANISM: Homo sapien
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S-09-543-679A-2905
Sequence 2905, Application US/09543679A
Sequence 2905, Application US/09543679A
Patent No. 7034007
Patent No. 7034007
Patent No. 7034007
APPLICANT: NYCE, Jonathan W.
APPLICANT: NYCE, JONATHAN W.
COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH
OF AIRWAY DISORDERS ASSOCIATED WITH
OF AIRWAY DISORDERS ASSOCIATED WITH
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                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2905:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
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                                                                                                                                                                                                                         APPLICATION NUMBER: 60/127,958 FILING DATE: 1998-08-03 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSES: EPGENESIS PHARMACEUTICALS,
STREET: 7 Clarke Drive
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                                                                                                                                               REFERENCE/DOCKET NUMBER: EPI-0067191b TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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LENGTH: 14978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                              TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
                                                                                                                                                                                        NAME: Amzel, Viviana REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NJ
COUNTRY: USA
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Best Local Similarity
Matches 1248; Conserv
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                                                                                             TTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACT
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AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA 115
                                          CTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT
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APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANTON: SOLUBLE ZALPHA11 CYTOKINE REFILE REFERENCE: 00-02
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 966
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (966)
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Sequence 29, Application US/09313942

PATENT NO. 6472179

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)... (2352)
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RESULT 12 US-10-282-162-29 ; Sequence 29, Application US/10282162 ; Patent No. 6927044 ; GENERAL INFORMATION:

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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAK:
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
INVMBER OF SEG ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
SEG ID NO 29
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; NAME/KEY: CDS
; LOCATION: (1)...(2352)
US-10-282-162-29
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Best Local S
Matches 951
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TYPE: DNA
ORGANISM: Homo
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                                                              GAAACCTGATCCTCCACATATTAAAAACCTCTCCCTTCCACAATGATGACGACGTATATGTdCA 794
                                                                                                                  CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCCTTTAACTTCCCGTGT
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               ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA 854
                                                                                                                                                                     CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACACAGTGTCCAAATAATGGT
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ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA 143:
                                                                                                     CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
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99.9%;
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US-09-313-942-31
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Best Local
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT APPLICATION NUMBER: 09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 00/101,858
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
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LENGTH: 2382
TYPE: DNA
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
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                                                                                               GTCTGCTGTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG 494
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                                                                     GTCTGCTGTGACTGAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG
                                                                                                                                                                                                                                                                                                                                               TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTTCGATCAAT
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Pred. No. 0;
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GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND MET

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-B-US

CURRENT APPLICATION NUMBER: US/10/282,162

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: 09/787,835

PRIOR APPLICATION NUMBER: 09/787,835

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: PCT/US99/22045

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 31

LENGTH: 7182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-282-162-31
                                                                                                                                               TYPE: DNA

ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2379)
IS-10-282-162-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/10282162 Patent No. 6927044
                                                                                      Matches
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     LENGTH: 2382
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                                     CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAACCTCTG
                    CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG
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; Sequence 2679, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G.
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2679
LENGTH: 701
TYPE: DNA
ORGANISM: Human
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Search completed: July 8, 2006, 01:19:24 Job time: 302 secs

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Perfect score:
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         Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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US-10-172-118-633
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US-10-342-887-633
US-10-342-887-634
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US-09-971-392-846-109
US-10-850-568-3
112 US-10-745-586-32
110 US-10-850-270-3
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9 US-10-278-698-6
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US-11-182-384A-3
US-11-183-599A-3
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Sequence 3, Appli
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Sequence 16, App
Sequence 3856, Ap
Sequence 633, App
Sequence 633, App
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Sequence 58, Appli
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APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Vita, Natalio
TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
FILE REFERENCE: IVD924 US CNT 1
CURRENT APPLICATION UMBER: US/11/185,230
CURRENT PILING DATE: 2005-07-18
                                                                                                                                                                                                               Query Match 86.6
Best Local Similarity 99.9
Matches 1248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
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PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                               GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
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PRIOR APPLICATION NUMBER: 09/077,817
PRIOR FILLING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILLING DATE: 1996-11-07
NUMBER: OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 4009
TYPE: DNA
ORGANISM: Homo sapiens
US-11-182-384A-3
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US-11-182-384A-3
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Publication No. US20060035855A1
GENERAL INFORMATION:
APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Laurent, Patrick
APPLICANT: Vita, Natallo
TITLE OF INVENTION: Purified polypeptides having
FILE REFERENCE: IVD924 US DIV 2
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Best Local Similarity
Matches 1248; Conserv
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CURRENT FILING DATE: 2005-07-15
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                      GAAACCTGATCCTCCACATATTAAAAAACCTCTCTCCTTCCACAATGATGACCTATATGTGCA
                                                                                        CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
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                                                                     CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
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; TYPE: DNA; ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens US-11-183-599A-3 Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 135 CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194	APPLICANT: Laurent, Patrick APPLICANT: Laurent, Patrick APPLICANT: Laurent, Patrick APPLICANT: Laurent, Patrick APPLICANT: Vita, Natalio TITLE OF INVENTION. Purified polypeptides having IL-13 receptor activity FILE REFERENCE: IVD924 US DIV 1 CURRENT APPLICATION NUMBER: US/11/183,599A CURRENT FILING DATE: 2005-07-15 PRIOR APPLICATION NUMBER: 09/077,817 PRIOR APPLICATION NUMBER: 09/077,817 PRIOR APPLICATION NUMBER: PCT/FR96/01756 PRIOR FILING DATE: 1998-09-14 PRIOR APPLICATION NUMBER: PCT/FR96/01756 PRIOR FILING DATE: 1996-11-07 SOFTWARE: PatentIn version 3.3 SEQ ID NO 3 LENGTH: 4009		1215 AGAAATGTTTGGAGACCAGAATGATGATGATGCTCTGCACTGGAAGAAGATGCTATGA	OY 103 CIGNATIANI INSACCIONALIMINATION DE LIGITATION DE L'ENTRE L'OYA 1011 CTGGAGTAATTGGAGCCAAGAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT 1070 1011 CTGGAGTAATTGGAGCCAAGAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT 1070 OY 1095 AACCATGTTACTCATTGTTCCAGTCATCGTCGCAAGTGCAATAGTACTCCTGCTTTA 1154 1071 AACCATGTTACTCATTGTTCCAGTCATTCGTCGCAAGTCATAGTACTCCTGCTTTA 1130 OY 1155 CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGGCAAGATTTTTAA 1214 ON 1131 CCTAAAAAGGCTCAAGATTATTATTATTCCCTCCAATTCCTGATCCTGCCAAGATTTTTTAA 11100 DD 1131 CTTAAAAAGGCTCAAGATTATTATTATTCCCTCCAATTCCTGATCCTGGCAACATTTTTTTAA 11100	795 ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA
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ACCATGTTACTCATGTTATTATTATTATTATTATTATCCCTGCAGTGCAGAGAGTACCGCAGGTTCTTAA CCTAAAAAGGCTCAAGATTATTATTATTATTATCCCTCCAAGTTCCTGGCAGTCCTGGCAGATTCCTGGCAGATTCCTGGCAGATTCCTGGCAGATTTTTAA [CTAAAAAGGCTCAAGATTATTATTATTATCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA [CTAAAAAGGCTCAAGATTATTATTATTATCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA AGAAAATGTTTTGGAGACCAGAATGATACTCTGCACTGGAAGAAGTACGACATCTATGA [[]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]	831 CAGCCAAACTGAGACACATAATGTTTCTACGTCCAGAGGGCTAAATGTAGTACAGA 890 915 ATTTGAGAGAAATGTGTGTAGATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC 974	735 GARACCTGATCCTCCACATATTAAAAACCTCTCCACAATGATGATGACCTATATGTGCA 794	531 CCTGGAAAAATTCAATGTGAAAACATCTTTAAAGACAAGCCAATAATTCCGGTGT 590 615 CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACAGGGTCCAAATAATAGT 674	435 GTCTGCTGTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG 494	195 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 254 171 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 230 255 TTTTAGTCATTTTGGCGACAAACAAACAAAATAGAAAATAGCTCCGGAAACTGTACGTCAAT 314 231 TTTTAGTCATTTTGGCGACAAACAAACAAAAAAAAAAAA

QY 315 AGAAGTACCCCTGAATGAGAGGATTTGTCT	Qy 255 TTTTAGTCATTTTGGCGACAAACAAGATAA	Qy 195 CACAGTAATATGGACATGGAATCCACCCGA	Qy 135 CGCGCCTACGGAAACTCAGCCACCTGTGAC	Query Match 86.6%; Score 1198; D) Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches	NAME/KEY: CDS LCCATION: 431323 SEQUENCE DESCRIPTION: SEQ ID NO: 8 US-10-671-997-8	TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FRAGMENT TYPE: linear FEATURE:	SEQUENCE CHARACTERISTICS: LENGTH: 4038 base pairs TYPE: nucleic acid TYPETHENESS: single	o 0	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 09/545,002 FILING DATE: 06-APR-200 APPLICATION NUMBER: US 08/969,125	T APPLICATION DATA: PPLICATION NUMBER: US/10/671, PRICATION STATE 29-Sep-2003 LASSIFICATION: CINEROMN	COMPUTER: ISM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPATING SYSTEM: PC-DOS/MS-DOS COFTMADE: MS WORT	STATE: WIRDING STATE: WIRDING COUNTRY: U.S.A. ZIP: 22201.4714 COMBUTED DEADABLE FORM.	DENCE ADDRES ESSEE: NIXON ET: 1100 NOF	APPLICANT: BONNEFOY, JEAN-YVES APPLICANT: BONNEFOY, JEAN-YVES GAUCHAT, JEAN-FRANCOIS FITTLE OF INVENTION: SUBSTANCES AND NIMMER OF SPOIENCES.	US-10-671-697-8 US-10-671-697-8 ; Sequence 8, Application US/10671697 ; Publication No. US20040043921A1 ; GENERAL THORMATION.	Db 1311 TCAGTGATGGAGATAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA	335	OY 1275 GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA 374	314 299	CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTTATGGTA 254	TTGAGTGTCTCTGTTGAAAACCTCTG 194	1; Indels 0; Gaps 0;	υ Ω	0	Q			697		п О	.c.	THEIR USES	п О	1359		1334
RESULT 5 US-09-962-832-160	Db 1320 TCAGTGATGGAGATAATTTATTTTTACCTTCACTGTGAGAAGA 1368	1275 WANGCAMAC CANGGAGAAAC CGACLICIGIAG CGCIGAIAGAAAAC CGACHAGAAAC CGACLICIGIAG CGCIGAIAGAAAAC CGACHAGAAAAC CGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC 13	1215 HARAKIIGITIIGGAGACCAGAATIGATIGATIACICIGGACIGGA	1155 CCTAADAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA 1	سو سر	Qy 1035 CTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT 1094	QY 975 TTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACT 1034	Qy 915 ATTIGAGAGAAATGIGGAGAATACAICTIGITTCAIGGTCCCTGGIGITCTTCCTGATAC 974	QY 855 CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA 914	QY 795 ATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA 854	Qy 735 GAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGACCTATATGTGCA 794	Qy 675 CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT 734	Qy 615 CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGT 674	Qy 555 CCTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC 614	Oy 495 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG 554	Qy 435 GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG 494	ω	Db 300 AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA 359 Qy 375 GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA 434

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CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
SOFTMARE: Patentin version 3.0
SEQ ID NO 160
LENGTH: 4039
TYPE: DNA
ORGANISM: Homo sapiens
US-09-962-832-160
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Best Local Similarity
Matches 1248; Conserv
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APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cencer Gene Determination
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
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Patent No. US20020110821A1
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APPLICANT: Gene Logic, Inc.
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3856
LENGTH: 4039
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: Genbank Accession No. US2002
US-09-880-107-3856
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Best Local Similarity
Matches 1248; Conserv
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APPLICANT: Vockley, Jos
APPLICANT: Scherf, Uwe
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GAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC
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APPLICANT: Van't Veer, Laura
APPLICANT: Van't Veer, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 633
LENGTH: 4039
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Publication No. US20
GENERAL INFORMATION:
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Best Local Similarity
Matches 1248; Conserv
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APPLICANT:
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 001560
DATABASE ENTRY DATE: 2001-06-18
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
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Roberts, Chris
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5. US20030224374A1
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0; Mismatches
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RESULT 8
US-10-342-887-633
; Sequence 633, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Wan, Mao
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Noberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Hernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
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; PRIOR FILLING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 633
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match 86.6%; Score 1198; DB 10; Length 4039; Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 135 CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194	Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 8447 SOFTWARE: PatentIn version 3.0 SEQ ID NO 6046 LENGTH: 4039 TYPE: DNA ORGANISM: Homo sapiens US-10-843-641A-6046	ICATION NUMBER: US/09/9 NG DATE: 2001-09-28 ICATION NUMBER: US/09/9 NG DATE: 2001-10-02 ICATION NUMBER: US/09/9 NG DATE: 2001-10-02 ICATION NUMBER: US/09/9 NG DATE: 2001-10-03	PRIOR FILING DATE: 2001-09-25 PRIOR APPLICATION NUMBER: US/09/962,436 PRIOR APPLICATION NUMBER: US/09/962,436 PRIOR APPLICATION NUMBER: US/09/962,832 PRIOR APPLICATION NUMBER: US/09/962,832 PRIOR APPLICATION NUMBER: US/09/964,824 PRIOR FILING DATE: 2001-09-27	09/873,	ublication No. U\$20050 ENERAL INFORMATION: APPLICANT: Avalon Phar TITLE OF INVENTION: Ca TITLE OF INVENTION: S FILE REFERENCE: 689290 CURRENT APPLICATION CURRENT APPLICATION	Db 1321 TCAGTGATGAAATTTATTTTTACCTTCACTGTGACCTTGAGAAGA 1369 RESULT 9 US-10-843-641A-6046 : Sequence 6046. Application US/10843641A	1275 GAAGCAACCCAAGGAAACCGACTCTGTAGTGCTGATAGAAAACCIG	1215 AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA	QY 1155 CCTAAAAAGGCTCAAGATTATATATATCCCTCCAATTCCTGGCAAGATTTTTAA 1214 	Qy 1095 AACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTACTCCTGCTTTA 1154	Oy 1035 CTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT 1094
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1155 CCTAAAAAGGCTCAAGATTATTATATTCCCTCCCATTCCTGATCCTGGCAAGATTTTTAA 1214	CTGGAGTAATTGAGCCAAGAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACAT [ATGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAA CAGCCAAACTGAGAACTCTAATTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA		615 CTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGT 674	481 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCCTACTATTGGCACAGAAG 540 555 CCTGGAAAAATTCATCATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTC 614	GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTACCTGATGAAGTGTACCTGAGTGTACATGAAGTGTACCTAATGCATTTGGCACAACCTGAGGTACATGAAGTGTTCTTTGGTCCTGCTGTGACTGAAGTGTTCTTTGGCACAACCTGAGTACTTACT	GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAGGTGATCCTGA	315 AGAAGTACCCCTGAATGAGAGGAGTTTTGTCTGCAAGTGGGGTCCCAGTGTAGCACCAATGA 374	255 TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT 314	195 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 254

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GENERAL INFORMATION:

APPLICANT: Peterson, David P.

APPLICANT: Pearson, Cecelia I.

APPLICANT: Cocks, Benjamin G.

TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CEI

FILE REFERENCE: PA-0029 US

CURRENT APPLICATION NUMBER: US/09/971,392

CURRENT FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: 60/237,652

PRIOR FILING DATE: 2000-10-03
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US-09-971-392-58
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SEQ ID NO 58
LENGTH: 4466
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NUMBER OF SEQ ID NOS: 260
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NAME/KEY: misc_feature
OTHER INFORMATION: Template ID: 331428.2
NAME/KEY: unsure
LOCATION: 1874-2179, 4212, 4229, 4239, 4254,
OTHER INFORMATION: a, t, c, g, or other
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ORGANISM: Homo sapiens
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APPLICANT: MCCOY, J
APPLICANT: LaVallie
APPLICANT: Collins-
APPLICANT: Evans, C
APPLICANT: Merberg,
                                                                                                                                                                                                                                                                                    Sequence 109, Application No. US20 GENERAL INFORMATION:
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert German, Michael R.
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                                                Spaulding, Vikki
Wong, Gordon G.
Clark, Hilary
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McCoy, John M.
LaVallie, Edward R.
Fechtel, Kim
Howes, Steven H.
Resnick, Richard J.
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APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 109
LENGTH: 3880
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Best Local Similarity
Matches 1239; Conserv
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1338)
US-10-036-568-3
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APPLICANT: Wilson, Tracy
APPLICANT: Wilson, Nicos A.
APPLICANT: Wilson, Douglas J.
APPLICANT: Hilton, Douglas J.
APPLICANT: Hocalf, Donald
APPLICANT: Zhang, Jian G.
TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND
TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND
TITLE OF INVENTION: ENCODING SAME
FILE REFERENCE: Davies CC
CURRENT APPLICATION NUMBER: US/10/036,568
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US/09/051,843
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1383
TYPE: DNA
CDCANTISM: Human II.-13 receptor alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10036568 Publication No. US20020090682A1
                    GAGTCTAACACGGACCAAGGAGTTTAACACGTGCGGCCGGGTTCCGAGGCGAGAGGCTGC
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                                  GTACTCCTGCTTTACCTAAAAAAGGCTCAAGATTATTATATTTCCCCTCCAAGTTCCTGATCCT
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GGCAAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAG 1260
                                                                TCCACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATA
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Tracacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POI
FILE REFERENCE: GI 6011-18X
CURRENT APPLICATION NUMBER: US/10/745,586
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
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US-10-745-586-32
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                                                                                                                                                                                                                                                                                                                                                                               Matches 1238;
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Best Local
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TYPE: DNA
ORGANISM: Homo
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RESULT 14

US-10-850-270-3

; Sequence 3, Application US/10850270
; Publication No. US20050058645A1

; GENERAL INFORMATION:
; APPLICANT: ANRAD Operations Pty Ltd (for all APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Mean, Manuel(US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Novel peptides
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CURRENT FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: AU PS1301
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: AU 2003900437
PRIOR FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1284
TYPE: DNA
ORGANISM: human
FEATURE:
NAME/KEY: CDS
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COTER INFORMATION:
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315 AGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGGTCCCAGTGTAGCACCAATGA 374	255 TTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAAT 314 	195 CACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTA 254 	135 CGCGCCTACGGAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAAC	uery Match 79.2%; Score 1096; DB 9; Length 1572; set Local Similarity 99.8%; Pred. No. 0; atches 1246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	LENOTH: 1572 TYPE: DNA ORGANISM: Homo sapiens 0-278-698-6	CURRENT FILING DATE: 2002-10-23 NUMBER OF SEQ ID NOS: 1050 SOFTWARE: PatentIn version 3.2 SEQ ID NO 6	ICANT: Haupl, Thomas B OF INVENTION: Nucleic Acid Array REFERENCE: 030027US ENT APPLICATION NUMBER: US/10/278,698	Publication No. US20050037344A1 PENERAL INFORMATION: APPLICANT: PathoArray GmbH APPLICANT: Stuhlmuller, Bruno	SSULT 15 3-10-278-698-6 Sequence 6, Application US/10278698	1335 TCAGTGA 1341 1278 TCAGTGA 1284	1275 GAAGCAAACCAAGGAAGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTC 1334 	1215 AGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGA 1274	1155 CCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAA 1214	1095 AACCATGTTACTCATTGTTCCAGTCATGCTCGCAGGTGCAATCATAGTACTCCTGCTTTA 1154	035 978	975 TTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACT 1034 	58	CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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US-11-266-748A-15283

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US-11-266-748A-27658

US-11-266-748A-27658

US-11-266-748A-12643

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1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8
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16780,	Sequence 1093, Ap	Sequence 33381, A	Sequence 40071, A	Sequence 10524, A	Sequence 4763, Ap	Sequence 481172,	Sequence 390454,	Sequence 339154,	Sequence 287725,	Sequence 222027,	Sequence 206504,	Sequence 23747, A		Sequence 7949, Ap	Sequence 22993, A	Sequence 15541, A	Sequence 3444, Ap	Sequence 24102, A	Sequence 14434, A	Sequence 24182, A

ALIGNMENTS

Johnston, Patrick Mulligan, Karl Paul

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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25722
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PRILING DATE: 2004-11-03
PRIOR PRILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
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PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
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LENGTH: 2139
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Best Local Similarity 99.9
Matches 1248; Conservative
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/602,276
PRIOR APPLICATION NUMBER: US 60/602,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PRIOR DATE: 2005-03-14
PRIOR PRIOR DATE: 2005-03-18
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US-11-266-748A-56241
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SEQ ID NO 56241
LENGTH: 4006
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Best Local Similarity
Matches 1248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56241, Application US/
Publication No. US20060134663A1
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APPLICANT: Mulligan, Karlick
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION UNMERS: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG
                                                                                      GTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTG
                                                                                                                                               GAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAAAGGTGATCCTGA
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RESULT 3
US-11-266-748A-185183
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paurick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray
TITLE OF INVENTION: Methods of Using the Sam
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
                                                                                                                                                                   Sequence 185183, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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; LOCATION: (2177)...(2186)
; OTHER INFORMATION: n is
US-11-266-748A-185183
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Best Local Similarity
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SEQ ID NO 185183
LENGTH: 2741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1520)..(1834)
OTHER INFORMATION: n is a
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OR APPLICATION NUMBER: EP 04105482.6

OR FILING DATE: 2004-11-03

OR APPLICATION NUMBER: EP 04105483.4

OR FILING DATE: 2004-11-03

OR PILING DATE: 2004-11-03

OR APPLICATION NUMBER: EP 04105507.0

OR APPLICATION NUMBER: EP 04105485.9

OR APPLICATION NUMBER: EP 04105484.2

OR FILING DATE: 2004-11-03

OR APPLICATION NUMBER: EP 04005484.2

OR FILING DATE: 2004-11-03

OR APPLICATION NUMBER: US 60/662,276

OR APPLICATION NUMBER: US 60/700,293

OR APPLICATION NUMBER: US 60/700,293

OR PILING DATE: 2005-03-16

OR PILING DATE: 2005-03-16

OR PILING DATE: 2005-03-16
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ATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATAC
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                                                         CAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGA
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55615-0.02 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PRICING DATE: 2004-11-03
PRIOR PRICING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER: DE PRIOR FILING DATE: 2005-07-18
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                                 Query Match
Best Local Similarity
Matches 973; Conserv
                                                                                                                                              SOFTWARE: PatentIn version
SEQ ID NO 192679
LENGTH: 975
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                                   Conservative
                                                 99.9%;
                                Score 923; DB Pred. No. 0; 0; Mismatches
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RESULT 5
US-11-266-748A-226550
; Sequence 226550, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Mathods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR TILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-226550
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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CAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGT
                                                                                                                                                                                                                                 GCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAG
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Mulligan, Karl
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Pred. No. 0;
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                   ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (60)..(60)
OTHER INFORMATION: n is
US-11-266-748A-54658
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US-11-266-748A-54658
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
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SEQ ID NO 54658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                  TYPE: DNA
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RESULT 7
US-11-266-748A-73628/c
Sequence 73628, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
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Pred. No. 0;
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CURRENT APPLICATION UNMERE: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-07-18
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Best Local Sim:
Matches 811;
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ORGANISM: Homo Sapiens
ORGANISM:
PRATURE:
PRATURE:
NAME/KEY: misc feature
LOCATION: (30)...(30)
OTHER INFORMATION: n is
US-11-266-748A-73628
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SEQ ID NO 73628
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                                                                                                     AAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGCCA
                                                                                                                                                                       GAATACATCTTGTTTCATGGTCCCTGGTGTTCTTCCTGATACTTTGAACACAGTCAGAAT
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                   AGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTACTCATTGT
                                                                                   AAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAATTGGAGCCA
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ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (30) . (30)
OTHER INFORMATION: n is a, c
US-11-266-748A-107924
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APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (31918)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 107924
LENGTH: 1294
TYPE: DNA
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Best Local Similarity
Matches 811; Conserv
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           GAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAATGCAGGAAA
                                                                                           ATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCCTTTGATCTGACCAAAGT
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILLING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
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PRIOR APPLICATION NUMBER: EP 04105485.9
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
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ORGANISM: Homo Sapiens
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                                                                                GAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACCAAGGAGGA 1293
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APPLICANT: Harkin, Paul
APPLICANT: HANKIN, Paul
APPLICANT: Mullidan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR RELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105485.9
PRIOR APPLICATION NUMBER: ED 04105485.9
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR RILING DATE: 2005-07-18
PRIOR RILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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Matches
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Publication No. US20060134663A1
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NAME/KEY: misc_feature
LOCATION: (872)..(872)
OTHER INFORMATION: n is
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NAME/KEY: misc feature
LOCATION: (902)..(902)
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version SEQ ID NO 73627
                                                        LOCATION: (81)...(168)
OTHER INFORMATION: n is a
FEATURE:
NAME/KEY: misc feature
LOCATION: (170)...(171)
OTHER INFORMATION: n is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
(81)..(168)
                                                                                                                                                                                                       LENGTH: 1297
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                            OTHER INFORMATION: n is
     NAME/KEY: misc feature
LOCATION: (174)..(174)
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Sequence 107923, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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Best Local Similarity
Matches 328; Conserv
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (1125)...(1125)
OTHER_INFORMATION: n is
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LOCATION: (184)..(184)
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Pred. No. 2.6e-140;
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; NAME/KEY: misc feature
; LOCATION: (1147)...(1187)
; OTHER INFORMATION: n is
US-11-266-748A-107923
  Matches 328;
              Query Match
Best Local Similarity
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SEQ ID NO 107923
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NUMBER OF SEQ ID NOS: 48399
SOFTWARE: Patentin version
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LOCATION: (1133). (1133)
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NAME/KEY: misc_feature
LOCATION: (60)...(60)
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OTHER INFORMATION: n is
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LOCATION: (174)..(174)
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LOCATION: (81)..(168)
OTHER_INFORMATION: n is
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LOCATION: (1011)..(1121)
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LOCATION: (170)..(171)
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APPLICATION NUMBER: EP 04105507.0
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SEQ ID NO 126438
LENGTH: 1297
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
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                                     NAME/KEY: misc feature LOCATION: (165)..(165) OTHER INFORMATION: n in
                                                                                                                        NAME/KEY: misc feature
LOCATION: (158)..(160)
OTHER INFORMATION: n i:
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NAME/KEY: misc_feature
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RESULT 14

US-11-266-748A-51095
Sequence 51095, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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Best Local Similarity 99.78;
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OTHER INFORMATION: n is
FEATURE.
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LOCATION: (1127)..(112)
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LOCATION: (1124)..(1124)
OTHER_INFORMATION: n is a,
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LOCATION: (177)..(287)
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OTHER INFORMATION: n is a,
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LENGTH: 583

TYPE: DNA

ORGANISM: Homo Sapiens
FEATURE:

NAME/KEY: misc feature
LOCATION: (572)..(572)
OTHER IMFORMATION: n is
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US-11-218-305-11789
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US-11-218-305-11789
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
                                                                         Best Loc
Matches
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APPLICANT: MONSANTO TECHNOLOGY,
APPLICANT: McLaird, Paul L.
                                                                                                                                                                                                                                 SOFTWARE: PatentIn version SEQ ID NO 11789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11789, Application US/11218305 Publication No. US20060141495A1
                                                                                                                                                                                                                                                          APPLICANT: McLaird, Paul L.
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Corn.
FILE REFERENCE: 38-21 (53660)B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
NUMBER OF SEQ ID NOS: 25043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 63;
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                                                                                                                  Query Match
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Best Local :
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SOFTWARE: PatentIn version 3.3
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Search completed: July 7, 2006, 23:52:18 Job time: 205 secs

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Result
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         GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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ADL71812
ADL82843
ADN04504
ADN062575
ABM82441
AEC31473
AEE93788
AEE93788
ADL71811
ADL71811
ADL718114
AAB19808
ADL97531
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AAW24973
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Aaw24973 Human int
Aab19807 Humán int
Adl19812 Humán int
Adl82843 Human pro
Adn04504 Antipsori
Adn62575 Humán int
Adm82441 Tumour-as
Aec31473 Humán III-
Aee93788 Humán III-
Aee93788 Humán int
Adf17813 Humán int
Adf17813 Humán int
Adf17814 Humán int
Adf17814 Humán int
Adm97331 Pancreati
Adw97331 Pancreati
Auw92208 III-13/II-
Abw02181 Human III-
Abw02181 Human III-
Abw02181 Humán III-
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AAW36616	AAU69141	AAU69138	AAU69136	ADZ58697	AAR22217	AAR22211	AAR22212	AAU69135	ADO26844	ADQ65618	ADP84616	ADP84617	AAW58987	AAB90678	ADX97888	AAW09821	AEC31480	AEC31486	AEC31478	AEC31484	AEC31482
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ALIGNMENTS

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23-OCT-1995;
22-DEC-1995;
                                                                                                                                                                                                                                Key
Peptide
                       23-OCT-1996;
                                       01-MAY-1997.
                                                      WO9715663-A1
                                                                            Domain
                                                                                            Domain
                                                                                                          Region
                                                                                                                                           Domain
                                                                                                                                                                         Modified-site
                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                       NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine; allergy; asthma; therapy.
                                                                                                                                                                                                                                                                                              Human interleukin-12 receptor alpha chain NR4
                                                                                                                                                                                                                                                                                                               15-JUL-1997
                                                                                                                                                                                                                                                                                                                               AAW09822;
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                                                                                                                            Modified-site
                                                                                                                                                          Modified-site
                                                                                                                                                                                                                 Protein
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95AU-00006135.
95AU-00007276
                       96WO-AU000668
                                                                              /label=
367. .42
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                           /label= N-glycosylation
326. .330
                                                                     'label= Cytoplasmic_tail
                                                                                                                                           /label= N-glycosylation_site
119. .342
                                                                                                                                                                                /label= Extracellular domain
/note= "Ig-like domain"
                                                                                                                                                                                                                       /label= Sig_peptide
                                                                                                                                 'label= Haemoreceptor_receptor-domain
                                                                                                                                                                 'label= N-glycosylation site
                                                                                                                                                                                                       label= Mat_protein
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                                                                                   Transmembrane_domain
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RESULT 2
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Best Local :
                            AAW24973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822), designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain. The human NR4 amino acid sequence was adduced from a composite DNA sequence (AAT66165) derived from bone marrow cDNA clones. Recombinant NR4, or fusion proteins including NR4, can be produced in transformed host cells. The receptor molecules and their components are useful in the development of a range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor, esp. for the development of cpds. capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of allergy,
  22-JUN-1998
                                                        AAW24973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding animal haemopoietin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated
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                                                        standard;
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Pred. No. 4
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4.6e-212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CC This sequence represents interleukin-13 (II-13) alpha receptor. The CC invention relates to new purified peptides comprising 380 or 427 amino CC acid sequences, which are receptors for interleukin-13 (II-13); the 380 CC and 427 am proteins are designated II-13R beta and alpha respectively. CC The II-13R beta has high affinity for II-13R while II-13R alpha has low CC affinity, but acquires high affinity when associated with the II-4 CC receptor. Nucleic acids encoding II-13R beta and alpha are used as CC diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal CC anomalies. They are also used for production of recombinant II-13R beta and alpha which can be used as II-13 antagonists, specifically to regulate II-13-induced responses for treatment of inflammation and CC regulate II-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of II-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of CI I-13R receptors; when coupled to a toxin also for treatment of coverproduction of II-13R. Cells that express II-13R at the surface are used to identify ligands and modulators of II-13R
                                                                                                                                                                                                                                                                                                                                                               Matches 426;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified human interleukin-13 receptors - and related nucuseful for diagnosis and treatment of inflammation, allergy,
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                        DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
                                                                      QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
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99.8%;
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Pred. No. 4.7e-211;
0; Mismatches 0;
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359 300 240 239

299

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RESULT 3
AAB19807
ID AAB1
XX AAB1
AC AAB1
XX INTE
YI PEPT
YI PEPT
YI DOMA
YI OTAL
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The present sequence is that of a protein capable of binding human interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated from a human activated tonsilar cDNA library. This IL-13 receptor alpha-1 polypeptide can be used to inhibit IL-13 or IL-4 induced IGE synthesis in B cells, useful in the treatment of diseases in which IGE or Th2
                                                                                                                                                                         Claim
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l for treating atopy, atopic dermatitis, allergies, rhinitis,
a, asthma or AIDS.
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BONNEFOY J.
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tis; allergy; rhinitis; eczema; asthma; AIDS;
; antiasthmatic; antiallergic; therapy; diagnosis.
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Best Local
                                                                                                                                                                 Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; eczema; asthma; AIDS; gene therapy; interleukin; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation plays a role, e.g. atopy, atopic dermatitis, allergy, rhinicis, eczema, asthma or AIDS. Antibodies raised against the polypeptide are useful for detecting II-13 and II-4 receptor or parts of them which have been shed from cells as a result of disease, e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma, lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease, sporiasis, urticaria, ulcerative colitis, Crohn's disease, Sjogren's
              Domain
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                                                                                                                                        Homo sapiens
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Query Match
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Matches 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
NLKKASQ 426
                                                                                                                                                   GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
                                                                                                                                                                                                               DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
                                                                                                                                                                                                                                       DDLYVQMENPQNF ISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
                                                                                                                                                                                                                                                                                                      QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
                                                                                                                                                                                                                                                                                                                              QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEWPARLCGLWALLICAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGA&S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a disease in which interleukin (IL)-13 and IL-4 cause adverse e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, ast comprises administering a polypeptide or soluble polypeptide.
                                                                             IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
                                                                                                                            GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
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                                        IVLLLYLKRIKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
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97US-00969125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2309.5; DB 8
Pred. No. 4.7e-211;
0; Mismatches 0;
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                                                                                                                                                                                                                                antigen unresponsiveness, selective 1gA deficiency, selective 1gM deficiency, selective 1gM deficiency, selective 1gM deficiency with hyper 1gM, transient hypogammaglobulinemia of infancy, Burkitt's 1ymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadremocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human.
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Fig 45; 695pp; English.
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                                                                                                                                                                                                                      screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRO proteins are useful for diagnosing and treating a B cell related rider, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-329389/30
DB; ADL82842.
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NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
                          NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
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Pred. No. 4.7e
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                                                                                                                        2309.5; DB 8;
No. 4.7e-211;
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N-PSDB;
                                                                                                                                                                               The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                               Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis
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DB; ADN04503.
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Pred. No. 4.7e-211;
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                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
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Human; receptor; cytokine; interleukin 13 receptor alpha 1 chai: IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; asthicancer; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; multiple sclerosis; Alzheimer's dispuse erythematosus; thyroiditis; diabetes; uveitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; ulcerative crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis Lyme disease; tuberculosis; malaria; leichmaniasis.
                                                                                                                                                                                        Human interleukin 13 (IL-13) receptor alpha 1 chain.
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    toxoplasmosis; listeriosis; leprosy; leichmaniasis.
                                                                                                                            chain; lasthma;
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06-APR-2000; US6743604-B1 13-DEC-1996; 12-NOV-1997; sapiens. 2000US-00545002 96GB-00025899. 97US-00969125. /note= "Signal 27. .427 Location/Qualifiers "Mature protein claimed peptide 'n claim

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cc which encodes the mature form of a polypeptide capable of binding human CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated CI IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are CC a vector comprising the nucleic acid molecule and a host cell comprising the nucleic acid molecule and a host cell comprising CC the vector. The nucleic acids are useful as probes or primers or in the CC analysis of allelic variation. The polypeptides are useful for binding CC human IL-13 and/or binding human IL-4 and act as inhibitors by CC interfering with the interaction between human IL-13 or IL-4 and their CC interfering with the interaction between human IL-13 or IL-4 and their CC diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema, CC asthma, AlDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease, CC fupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis, CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis, CC urdicaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis, CC used for producing antibodies, which can be used for diagnosing diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 426
ABM82441;
                                                    ABM82441 standard;
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                                                 protein; 427
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                                                                                                                                                                                                                                                                                                                                                                                                                    IGKKRNSTLYITMLLIVPVIVAGAI
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NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP

PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG

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                                                                                                                                                                                TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, particularly cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                  polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cutumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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                                                                               Conservative
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Pred. No. 4.7e-211;
0; Mismatches 0;
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                                                                                                                DB 8;
                                                                               Indels
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RESULT 9
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AC ABC3
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KW inte
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The invention relates to a novel nucleic acid molecule encoding a polypeptide. The fusion polypeptide consists (R1)x-(R2)y-F, where -231 and 24-231 of a fully defined sequence of 231 amino acids (ABC31472), which sequences may comprise 1-10 modifications, R2 is
                                                                                                                                                                                                 New nucleic acid molecules encoding polypeptides capable of binding interleukin-4 and interleukin-13, useful for diagnosing and/or treating asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-2004; 2004US-0548541P
17-AUG-2004; 2004US-0602139P
16-NOV-2004; 2004US-0628343P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-13 receptor; fusion protein; therapeutic; antiasthmatic; antiallergic; dermatological; antinflammatory; immunosuppressive; cytostatic; hepatotropic; anti-HIV; virucide; gastrointestinal-gen; antibacterial; fungicide; antiparasitic; antiulcer; antithyroid;
                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2005; 2005US-00067251
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RESULT 10
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XX Human
XX Monoc

AEE93788

standard;

protein;

NLKKASQ

427

23-FEB-2006

(first

entry)

Monoclonal antibody; IL-13 alpha receptor; cytokine;

Humani nterleukin-13 alpha receptor

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CC component, and x and y are each independently a positive integer 1. The F
CC is a multimerizing component, a serum protein, or a molecule capable of
CC binding a serum protein, where the multimerizing component is an
CC immunoglobulin-derived domain, a cleavable region (C-region), an amino
CC acid sequence between 1-500 amino acids in length, optionally comprising
CC at least one cysteine residue, a leucine zipper, a helix loop motif, or a
CC coil-coil motif. The immunoglobulin-derived domain is the FC domain of
CC IgG or the heavy chain of IgG. A fusion protein of the invention has
CC antiasthmatic, antiallergic, dermatological, antiinflammatory,
CC immunosuppressive, cytostatic, hepatotropic, anti-HIV, virucide,
CC gastrointestinal-gen, antibacterial, fungicide, antiparasitic, antiulcer,
CC antithyroid, and nephrotropic activity. The protein has a use in gene
CC therapy, and acts as an interleukin-antagonist. The methods and
CC compositions of the invention are useful for the diagnosis, prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of II-4 and/or II-13, such as asthma, atopic
CC dermatitis, lupus, nephritis, Garve's disease, hepatic fibrosis, HIV
CC and fungal infections. The present sequence represents human II-13
CC receptor alpha-1.
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Best Local S
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Pred. No. 4.7e-211;
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Lin LL,
                                                                                                                    Crystalline antibody useful for designing agent that interacts polypeptide, comprises anti-IL-13 antibody capable of binding s 13 polypeptide to which IL-4R polypeptide binds in vivo.
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           The invention relates to a crystalline antibody (1), where the antibody comprises an anti-interleukin (II)-13 antibody or its Rab fragment, and is capable of binding a site of an II-18 polypeptide to which an II-4R (interleukin-4 receptor) polypeptide binds in vivo. Also included are
                                                                                                                                                                                                                                                                                                         09-JUN-2004; 2004US-0578473P
09-JUN-2004; 2004US-0578736P
22-JUN-2004; 2004US-0581375P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic obstructive pulmonary disease; cystic fibrosis;
pulmonary fibrosis; allergic rhinitis; atopic dermatitis;
inflammatory bowel disease; Crohns disease; cirrhosis; scleroderma;
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SPROT; P78552.
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mmatic; Antiallergic; Cytostatic; Respiratory-Gen.;
                                                                                                                                                                                                                                               Parris
                                                                                                                                                                                                                               Mosyak
composition/complexes that comprises an antibody
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RESULT 11
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DT 23-M2
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AEF57817 standard;

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23-MAR-2006

(first

entry)

Anti-IL-13-antibody associated polypeptide SEQ ID antiasthmatic; dermatological; respiratory-gen.; i

immunosuppressive;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody comprises an anti-IL-13 antibody or a Fab fragment of an anti-IL-13 antibody in complex with IL-13 or IL-13 alpha receptor), use of a three-dimensional model of an antibody to design an agent that interacts with an IL-13, a software system/computer for storing/analyzing information relating to a structure of an IL-13 polypeptide bound to an antibody, modulating IL-13 activity in a subject, treating a subject having a condition associated with IL-13 activity, a method of
421
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                                                                          IVLLLYLKRIKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
                                                                                               IVLLLYLKRLKIIIFPFIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
                                                                                                                                                    GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
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                                                                                                                                                                                                                            DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
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Pred. No. 4.7e-211;
0; Mismatches 0;
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The invention describes an antibody, or its antigen-binding, that binds CC to interleukin (IL)-13. Also described are: a pharmaceutical composition CC comprising the antibody, or its antigen-binding fragment above and a CC pharmaceutical carrier; a nucleic acid that comprises a sequence that CC encodes a polypeptide that comprises a heavy chain immunoglobulin CC variable region or a light chain immunoglobulin variable region described CC above; a host cell comprising a nucleic acid sequence that encodes the CC antibody, or its antigen-binding fragment, above; providing a recombinant CC antibody; treating an IL-13-associated disorder; and detecting the CC useful for diagnosing, preventing, and/or treating IL-13 associated CC disorder, e.g. asthmatic disorders, atopic disorders, chronic obstructive CC pulmonary disease (COPD), conditions involving airway inflammation, CC conditions, autoimmune conditions tumors or cancers, viral infection, CC suppression of expression of protective type 1 immune responses, allergic finities, or inflammatory bowel disease. This is the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Donaldson DD, Liu ___
AM. Parris KD,
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09-JUN-2004; 2004US-0578736P
22-JUN-2004; 2004US-0581375P
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antiasthmatic; chronic obstructive pulmonary disease; respiratory-gen.;
infection; viral infection; virucide; autoimune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 37; 169pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide associated with anti-IL-13-antibodies of the invention.
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QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
                                                                                                                   PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
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Pred. No. 4.7e-211;
0; Mismatches 0;
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The invention relates to polypeptides capable of binding human interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The invention also relates to a method of treatment of a disease in which III3 and II4 cause adverse effects. The method is useful for treating a disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides of the invention are useful in raising antibodies. It is also useful in gene therapy. The present sequence is human interleukin-13 receptor alpha (II-13 Ralpha) mutant protein. Note: This sequence is not shown in the
                                                                                                                                                                                                                                                                        Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, astl or AIDS, comprises administering a polypeptide or soluble polypeptide.
                                                                                                                                                                                                                                    Claim
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RESULT 13
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AC ADF17
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Matches 425
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                                                                                                                                                                                                                                                                               ADF17835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, however it is constructed based on human IL-13 Ralpha protein shown as SEQ ID NO:9 in the specification.
                                                  22-MAR-2002;
03-FEB-2003;
                                                                                                   02-OCT-2003
                                                                                                                                                                                                                    Human IL-13 alpha 1 receptor
                                                                               21-MAR-2003; 2003WO-AU000352
                                                                                                                     WO2003080675-A2
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2003AU-00900437.
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                                                                                                                                                          pulmonary
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N-PSDB; ADF17834.
           20-MAY-2004
                              ADL71814;
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           (first
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New monoclonal antibodies against interleukin-13 receptor alpha, for treating fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic rhinitis, oncological conditions, asthma or inflammatory disorder.
                                         Or
                                                                                                  useful
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Disclosure; SEQ ID NO 4; 99pp; English.

13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used for treating certain conditions induced by IL-13. Specifically, it refers to annibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13 and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory system, such that it is involved in the induction of IgE, IgG4 and T-helper cells and accordingly is implicated in conditions from anaphylaxis to hay fever and asthma. As such, the present invention describes these novel antibodies as antiinflammatory, cytostatic, antiulcer, dermatological, antiallergic and antiasthmatic. The methods and compositions are useful for treating various disorders including fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic rhinitis, oncological conditions and chronic obstructive pulmonary disease. This polypeptide sequence is the human IL-13 alpha 1 receptor protein of the invention. invention relates toa novel antibodies that function as interleukin

AA;

99.2%; 99.5%;

No. 2.2e

2e-210; DΒ 7;

Length

427;

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1 MEWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
NLKKASQ 426
                                                   IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
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Pred. No. 2.2e
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protein;

427

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Query Match
Best Local Similarity
Matches 425; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS, comprises administering a polypeptide or soluble polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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12-NOV-1997; 97US-00969125
06-APR-2000; 2000US-00545002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page; 27pp; English.
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; asthma; AIDS; gene therapy; interleukin; receptor; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEWPARLCGLWALLLCAGGGGGGGG-APTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
                       DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
                                                                                                                        QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKÞSFNIVÞLTSRVKÞDÞÞHIKNLSFHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2302.5; DB 8
Pred. No. 2.2e-210;
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The present sequence is that of a claimed isolated polypeptide which is capable of binding human interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a

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RAESULT 15
AAB19808
ID AAB19908
XX AAB19808
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                                                                                                                                       Novel polypeptide capable of binding interleukin-13 or interleukin-4 useful for treating atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma or AIDS.
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                                                                                       4; -; 26pp; English.
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sequence (see AAB19807) deduced from isolated cDNA by having residue 130 as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13 creceptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells, useful in the treatment of diseases in which IgE or Th2 differentiation plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised against the polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of them which have been shed from cells as a result of disease, e.g. cancer, leukaemia, atopy atopic dermatitis, diabettes, rhinitis, cezema, asthma, lupus erythematosus, AIDS, thyroiditis, diabettes, the lammatory bowel disease, glomerulonephritis, ulcerative colitis, croming disease, Sjogren's syndrome and toxoplasmosis. Note: The present sequence is not shown in the specification but is derived from the IL-13 creceptor alpha 1 sequence given in figure 1 (see AAB19807)
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Search completed: July 8, Job time : 197 secs

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                                                                                                                                                                                                                                                                                                                            8, 2006, 01:38:58; Search time 41 Seconds
(without alignments)
999.716 Million cell
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Biocceleration
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Pred. No. score grea is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

Matches

43;

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ຫ	4	ω	2	1	No.	Result
161.5	162.5	163	165	170	172.5	172.5	172.5	173	176	180	180	183	185	186	189	189	189	190	197.5	202	205.5	207	228	229	269.5	294.5	318	1653	Score	
7.0	7.0	7.0	7.1	7.3	7.4	7.4	7.4	7.5	7.6	7.8	7.8	7.9	8.0	8.0	8.1	8.1	8.1	8.2	8.5	8.7	8.9	8.9	9.8	9.9	11.6	12.7	13.7	71.2	Match Length	* Query
1092	333	830	396	897	622	376	288	918	630	809	303	292	616	581	610	412	310	610	831	369	369	373	400	335	348	420	415	426		
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JX0312	S13684	I50455	S22909	A39255	A40144	A59405	B59405	A36337	I51086	I53269	177524	177525	A30304	I45971	A36116	A41070	A29884	A34631	JQ1655	A42565	I49280	A55718	S06945	A40267	JC7907	S21052	S12357	7	ID	
differentiation-st	granulocyte-macrop	prolactin receptor	interleukin-3 rece	cytokine receptor		prolactin redeptor	prolactin redeptor									prolactin redeptor	prolactin redeptor	lactogen receptor				interleukin-2 rece		interleukin-5 rece	=		'n,	IL-13Ralpha 1 prot		

45	44	43	42	41	40	39	38	37	36	35	34	33	32	ω H	30
134.5	135.5	139	139	140	141	142.5	144	144.5	145	146.5	149	154.5	156.5	157	157
5.8	ა. 8	6.0	6.0	6.0	6.1	6.1	6.2	6.2	6.2	6.3	6.4	6.7	6.7	6.8	6.8
557	286	634	508	638	638	917	918	1097	638	608	878	896	378	896	378
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interferon alpha/b	granulocyte-macrop	somatotropin recep	erythropoietin rec	somatotropin recep	somatotropin recep	glycoprotein 130 -	interleukin-6 sign	leukemia inhibitor	somatotropin recep	somatotropin recep	interleukin-3 rece	interleukin-3 rece	granulocyte-macrop	cytokine receptor	interleukin-3 rece

ALIGNMENTS

IL-13Ralpha 1 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: JC7773 A;Gene: il-13ralpha1 A;Accession: JC7773 A;Molecule type: mRNA A;Residues: 1-426 <PIE> R;Pierrot, C.; Beniguel, L.; Begue, A.; Khalife, J. Biochem. Biophys. Res. Commun. 287, 969-976, 2001 A,Tille: Expression of a functional IL-13Ralphal by A;Reference number: JC7773; PMID:11573960 A;Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251 C;Comment: This protein is an functionally binding protein involved in Genetics: Query Match Local 71.2%;
pal Similarity 73.3%;
313; Conservation Score 1653; DB 2; Length 426; Pred. No. 3e-121; 33; Mismatches 67; Indels 4; rat Ħ cells in B cell prolifera

밁 Ş 멂 Ş g 5 문 Š 밁 á 밁 δ 맑 á 419 359 299 299 239 ALFVQWKNPQNESSRCLSYEVEVNSTQTDSYNSNSLEVEEDKCQNSEFDRNMEGASCFIS 298 241 DLYVQWENPQNFISRCLFYEVEVNNSQTETH--NVFYVQEAKCENPEFERNVENTSCFMV 298 180 181 YFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHND 240 120 121 60 61 1 MEWPARLCGLWALLLCAGGGGGGGAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSN 60 ENLKKAS IIILFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQSKEETDSVVLI IIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLI 418 PGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGA 358 HIGCSFKLTKV-ESNYEHHNIQIMVKDNAGKIRPSYKIVSFTSNVKPGPPHIKHLFLKNG EGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQ 180 CSLRYFSHFDDQQDKKIAPETRRKKELPLNEKICLQVGSQCSTNESEKPSPLVKKCISPP 119 CSLWYFSHFGDXQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPP 120 MARPAWLGELLVLLLFAASLDQVALA-TEVQPPVTNLSVSVENLCTIVWTWSPPEGASPN 59 RRGSESAVTELQCTWHNLSYMKCSWLPGKNTSPDTNYTLYYWYSSLGKSLQCENIHREGQ 425 179

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text change 09-Jul-200
C;Accession: S21052; S21050; S21053; A46175; S78106; S78107
R;Murata, Y; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 recept A;Reference number: S21050; MUID:92121815; PMID:1732409
                                                                                                                                                                                                                                                                                                                                                                                                RESULT
S21052
                                        A; Molecule type: DNA
A; Residues: 1-395, 'I' < MU2>
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-420 < MUR>
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C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision
C;Accession: S12357
                                                                                                       A;Cross-references: UNIPROT:Q14633; UNIPARC:UPI00000729EE; A;Experimental source: clone lambda h5R.12
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A;Title: Molecular cloning and expression of the murine A;Reference number: S12357; MUID:91092260; PMID:2265612
A;Accession: S12357
                                                                                       A; Accession: S21050
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    A;Experimental
                                                                                                                                                                                                                                                                                                                                                                     interleukin-5 receptor alpha chain precursor (clone lambda h5R.12),
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A; Residues: 1-415 < TA
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Cross-references: UNIPARC:UPI0000179A7F; Experimental source: clone lambda h5R.27
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRLFPPVPAPKSNIKDL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPCRMPGR-WGEWSQPIYVGKERKS-LVEWHLIVLP---TAACFVLLIFSLICRVCHLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQN-FI&R
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Pred. No. 4.2e-17;
4; Mismatches 179
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                      EMBL:X61177; NID:g33839; PIDN:CAA43484.1;
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RESULT JC7907

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common cytokine C;Species: Gallu

Gallus

receptor us gallus

(chicken)

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chicken

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A;Cross-references: UNIPARC:UPI000006ED1C; R;Murata, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: S78107
A;Accession: S78107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI000006D11E; EMBL:X62156; NID:g36465; PIDN:CAA44081.1; C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prof;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S78106
A; Accession: S78106
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A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCB
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A;Residues: 1-128,'I',130-332,'K' <MU4>
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A; Residues: 333-420 <TAV>
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                                                                                                                                    TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLK
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ICHLWIKLFPPIPAPKSNIKDLFVTTN-
                                         --RLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL
                                                                                         DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLICK
                                                                                                                                                                                     PVSAFPIHCFDYEVKIHNTRNG----
                                                                                                                                                                                                                              PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN
                                                                                                                                                                                                                                                                            TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
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                                                                                                                                                                                                                                                                                                                                                                                                                      ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERICLQV----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:35:33 ; Search time 299 Seconds (without alignments) 1317.915 Million cell updates/sec

Title:
Perfect score:
Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-051-843D-4
2320
1 MEWPARLCGLWALLLCAGGG.....QTKEETDSVVLIENLKKASQ 426

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

patabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	31 373.	29 27	279			25 287.		23 294.			20 329			97	15								8 1878	7 192	19	5 2140	4 2291	3 2296.	2 2309.	1 2309.	 No. Score	Result
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ALIGNMENTS

	RA Hopk					RP NUCI				RN [4]							RL Submitt			RA Gauchat					RA Mile				OC Mami						DT 01-1	AC P78	ID T13	RESULT 1
3,1	Hopkins R.F., C	Altschul S.F.,	Klausner K.D., Collins	Strausberg R.L.,	MEDITNE=22388257.	NUCLEOTIDE SEQU	Submitted (SEP-1999)	M., Hisano	NUCLEOTIDE SEC	grot. citem.	receptor alpha chain.";	A cloning a	1 М.Ј., Таус	MEDLINE=97067184:	TISSUE=T-cell:		ed (JAN	H.P.,	P., Al		TISSUE=B-cell:	Lett.	alpha c	"Cloning of the	Miloux B., Laurent	MEDITUE-07165086.	NUCLEOTIDE SEQU		Mammalia: Eutheria:	Homo sapiens (1	e=IL13RA1;	A-1) (CD213	erleukin-13	07-MAR-2006, 61	NOV-1997, ii	P78552; 095646	13R1_HUMAN	
Usdin T.B.,	ີ 5		ollins	, Feingold E.A., Gr		SEQUENCE [LARGE SCALE	ť	Kuwano	SEQUENCE [MRNA].	211:23203-23210	chain.";	"cDNA cloning and characterization	bi N., Obiri N	04: PubMed=89105	ill:	MONA	to the	foy	S., Elson	lage	SEQUENCE (MRNA).	.63-166 (1997)	functional II	human IL-13R	cent P., Bonnin O.,		SEQUENCE [MRNA].	5;		_	Name=IL13RA1; Synonyms=IL13R,	13RA-1) (CD213a1 antigen).	receptor alpha	entry version 50	integrated into		STANDARD;	
Bonaldo M.F., Toshiyuki S		Buetow K.H.,	F.S., Wagner L.,	., Grouse	7933. DOT.	ALE MRNA].	the EMBL/GenBank/	••)(1330).	2000	ation of	.I., Puri	86:			EMBL/GenBank/DDBJ		No	Fenc			4/IL	lpha	O., Lupker				 oglires:		IL13RA;		1 chain	:			PRT; 4	
Casavant T.L., Scheetz T.E., S., Carninci P., Prange C.,	S.I., Wang J., Hsi	Schaefer C.F., Bhat N.K.,	Shenmen C.M., S	Grouse L.H., Derge J.G.,	03800		ık/DDBJ databases.					the human interleukin 13	Puri R.K., Modi W.S., Leonard W.J.;	10.1074/jbc.271.46.29265;			nk/DDBJ databases.		Wells T.,	Moser R Vama				ain and reconstitution with the	er J., Caput D., Vita N.,	1016/6001/6663 /1003/9101			a; vercebraca; Euceleoscomi; Primates: Catarrhini: Hominidae:				precursor (IL-13R-alpha-1) (IL-		/Swiss-Prot.		427 AA.	

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Ensembl; ENSG00000131724; H-InvDB; HIX0017008; -.
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EMBL;
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                                                                                                                                                                                                                                                      Glycoprotein; SIGNAL
                                                                                                                                                                                                                                                                InterPro; IPR002996; Cytkn_rcpt_B/G.
InterPro; IPR003532; Hempt_rcpt_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
Glycoprotein; Membrane; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                        CARBOHYD
                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kidney. Also found in B-Ce
- DOMAIN: The WSXWS motif ag-
- folding and thereby effici-
surface receptor binding
- DOMAIN: The box 1 motif is
                                                                                                                                                                                                                                                                                                               ; 300119; gene.
GO:0005898; C:interleukin-13 receptor complex; TAS.
GO:0005886; C:plasma membrane; TAS.
GO:0007166; P:cell surface receptor linked signal transdu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Binds IL13 with a low affinity. Together with IL41 can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor chain for IL4 signaling, but cannot replace the function of C in allowing enhanced IL2 binding activity.

SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL131 and possibly other components.

SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation.
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Y10659; CAA71669.1; -; mRNA.
Y09328; CAA70508.1; -; mRNA.
U62858; AAB37127.1; -; mRNA.
U83379; AAD00510.3; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                     HGNC:5974; IL13RA1.
                                                                                                                                                                                                                                                                                                                                                                                                        BC009960; AAH09960.1;
   PECIFICITY: Ubiquitous. Highest levels in heart, liver, muscle and ovary; lowest levels in brain, lung and Also found in B-cells, T-cells and endothelial cells. The WSXWS motif appears to be necessary for proper protein and thereby efficient intracellular transport and cell-
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/FTId=PRO_0000010939.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
WSXWS motif.
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                                    (Potential)
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CONFLICT
SEQUENCE
  Ensembl;
GO; GO:00
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                                       EMBL;
                                                                          Copyrighted
Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q5JSL4_HUMAN
Q5JSL4;
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                                                                                                                                                                                                                                                                                 Submitted (MAY-2005)
                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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folding
surface
DOMAIN:
  GO:0016021;
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O1-DEC-2001, integrated into Unil

O1-DEC-2001, entry version 1.

21-FEB-2006, entry version 23.

Interleukin 13 receptor, alpha 1
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagmer L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyaki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Eukaryota; Metazoa; C
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NLKKASQ
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Ensembl; ENSG00000131724; Homo sapiens.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoletin/interferon-class (D
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn_rcpt_B/G.
InterPro; IPR00392; Hempt_rcpt_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
Receptor; Transmembrane.
SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., I Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.; Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Membrane; single-pass type protein (By similarity).

DOMAIN: The WSXWS motif appears to be necessary folding and thereby efficient intracellular transurface receptor binding (By similarity).

DOMAIN: The box 1 motif is required for JAK inte
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tive Commons
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Pred. No. 6.3e
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Attribution-NoDerivs License
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Q598G2 HUMAN
Q598G2 HUMAN
PRELIMINARY; PRT; 426 AA.
AC Q59EG2;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 26-APR-2005, entry version 4.
DT 07-FEB-2006, entry version 4.
DE Interleukin 13 receptor, alpha 1 variant (Fragmen OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Euarchontoglires; Primates; COC Homo.
OX NCBI_TaxID=9606;
RN NUCLECTIDE SEQUENCE.
RC TISSUB-Aorta endothelial cell;
RN ONARA O., Nagase T., Kikuno F.R.;
"None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ date CC Distributed under the Creative Commons Attribution CC Distributed Under The Creative Commons Attributed Under The Crea
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Best Local S
Matches 424
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Ensembl; ENSG00000131724; Homo sapiens.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016896; F:hematopoietin/interferon-class
GO; GO:0004896; F:receptor activity; IEA.
InterPro; IPR002996; Cythr.rcpt_B/G.
InterPro; IPR003332; Hempt_rcpt_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoletin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR003996; Cytkn rcpt B/G.
InterPro; IPR003532; Hempt_rcpt_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maccarone P., Drinkwater C.C., Nash A.D.; "Cynomolgus monkey interleukin 13 receptor alpha Submitted (JUN-2003) to the EMBL/GenBank/DDBJ dat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                               DPGKI FKEMFGDQNDDTLHWKKYDI YEKQTKEETDSVVLI ENLKKASQ
DPGKIFKEMFGDONDDTLHWKKYDIYEKOTKEETDSVVLIENLKKASO
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                                                                                                                                                                                                                         YEVEVNNSQTETHNVFSVQEAKCQNPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL
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13 receptor alpha 1 (Fragment)
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Pred. No. 4.7e-154;
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RESULT 6 Q863Z6_PIG

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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2320
1 MEWPARLCGLWALL:
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(without alignments)
745.761 Million cell updates/sec
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No.	Score	Query Match	Length	BB	ID	Description
1	2320	100.0	426	2	US-09-688-286D-4	Sequence 4, Appli
2	•	99.5	427	N	-08-969-	equence
ω	2309.5	99.5	427	N	-09-545-002-	9
4		99.5	427	N	-09-949-016-	e 6094, A
ហ	~ 1	80.9	405	N	-09-828-995	e 50, App
თ	1875.5	80.8	793	N	1	æ
7	1875.5	80.8	793	Ν	-162	e 32,
8	1779.5	76.7	784	N	-942-	æ
9	1779.5	76.7	784	N	-162-	30
10	1769	. 76.2	322	N	-09-825-561A-	82
11	1696	ω.	424	2	-286D-	2
12	1265	4	233	Ν	-016-8	e 855
13	329	14.2	386	N	US-09-828-995B-61	e 61,
14	318	13.7	398	۲		Sequence 6, Appli
15	318	13.7	398	_		6
16	318	13.7	398	H	US-08-442-281-6	6, Appl
17	318	13.7	398	Н	1	6
18	318	13.7	415	۲	7-390-	5, Appl
19	318	13.7	415	1	US-08-442-282-5	Sequence 5, Appli
20	318	13.7	415	Н		5
21	318	13.7	415	_	9-727-	G G
22	318	13.7	415	2	US-09-886-319A-23	e 23,
23	310	13.4	365	N	8-995B-	99
24	304.5	13.1	561	N	-09-828-995B-	e 72,
25	303.5	13.1	561	N	-828-	Sequence 81, Appl
26	297	12.8	565	N	US-09-828-995B-75	75,

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181 YFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHND 240

YFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHND

EGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQ 180

EGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQ

180

CSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPP 120

241 DLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPG 300

B & B

121 121 δ

61 61

Query Match 100.0%; Score 2320; DB 2; Length 426; Best Local Similarity 100.0%; Pred. No. 5.7e-220; Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 MEWPARLCGLWALLLCAGGGGGGGAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSN	WS-09-688-286D-4 WS-09-688-286D 4 Pacent No. 6911530 Patent No. 6911530 GENERAL INFORMATION: APPLICANT: Willson, Tracey APPLICANT: Hilton, Douglas APPLICANT: Hilton, Douglas APPLICANT: Metcalf, Donald CORRENT APPLICATION NOWBER: US/09/688,286D CURRENT APPLICATION NOWBER: US/09/688,286D CURRENT APPLICATION NOWBER: AU PN6135 PRIOR APPLICATION NOWBER: AU PN7276 PRIOR FILING DATE: 1995-10-23 PRIOR APPLICATION NOWBER: AU PN7276 PRIOR APPLICATION NOWBER: AU PP2208 PRIOR APPLICATION NOWBER: AU PP2208 PRIOR FILING DATE: 1996-09-09 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PatentIn version 3.1 SEQ ID NO 4 LENGTH: 426 TYPE: PRT CORGANISM: human US-09-688-286D-4	27 296.5 12.8 420 2 US-09-886-319A-24 Sequen 28 296.5 12.8 420 2 US-09-949-016-958 Sequen 29 296 12.8 318 2 US-09-828-995B-69 30 296 12.8 512.7 380 1 US-08-609-572-4 Sequen 31 294.5 12.7 380 2 US-08-846-344-4 Sequen 32 294.5 12.7 380 2 US-08-846-344-4 Sequen 33 294.5 12.7 380 2 US-08-846-344-4 Sequen 34 294.5 12.7 380 2 US-08-846-344-4 Sequen 35 294.5 12.7 380 2 US-08-846-344-4 Sequen 36 294.5 12.7 420 1 US-09-301-808-4 Sequen 37 294.5 12.7 420 1 US-08-42-282-13 Sequen 38 294.5 12.7 420 1 US-08-42-281-13 Sequen 40 293.5 12.7 420 1 US-08-939-727-13 Sequen 41 293.5 12.7 420 1 US-09-949-016-8620 Sequen 42 287.5 12.4 383 2 US-08-841-751-2 Sequen 43 287.5 12.4 383 2 US-08-846-344-2 Sequen 45 287.5 12.4 383 2 US-08-846-344-2 Sequen
ngth 426; dels 0; Gaps 0; LCTVIWTWNPPEGASSN 60	genetic sequences encoding	Sequence 24, Appl Sequence 5958, Ap Sequence 69, Appl Sequence 78, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 13, Appl Sequence 2, Appli

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RESULT 2 US-08-969-125-9

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421 361 361 301

LKKASQ

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-969-125-9
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BONNEFOY, JEAN-YVES
    120 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
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                                               61 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
                                                                    60 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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Pred. No. 6.2e-219;
0; Mismatches 0;
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                                                                                     US-09-545-002-9
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  Query Match
Best Local Similarity
Matches 426; Conserv
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125
FILING DATE: 12-No. 6743604-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SUBSTANCES AND THEIR USES NUMBER OF SEQUENCES: 9
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                                                                                                                                                                 LENGTH: 427 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                    TELEPHONE: (703) 816-400
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                  NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/545,002 FILING DATE: 12-No. 6743604-1997 CLASSIFICATION: <Unknown>
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nilarity 99.8%;
Conservative 0
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  ; Score 2309.5;
; Pred. No. 6.2e-
0; Mismatches
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                       5; DB 2;
.2e-219;
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        Indels
                                             Length 427;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
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                                                                                                                                                                    Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
-09-949-016-6094
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                       LENGTH: 427
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 PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
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                                                                                                         MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
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Pred. No. 6.2e-219;
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US-09-828-995B-50
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 405
TYPE: PRT
ORGANISM: Canis f
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                  322
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DDKLWSNWSQEWSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPG
                                            EVNNSQTETNDIFYVEEAKCQNSEFEGNLEGTICFMVPGVLPDTLNTVRIRVRTNKLCYE
                                                          EVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYE
                                                                                                                          QIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEV 261
                                                                                                                                                                                  KCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSV 201
                                                                                                                                                                                                                                        RRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYM
                                                                                                                                                                                                                                                                                                     GGGGAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPET
                                                                                                       QIMVKDNARKIRPSFNIVPLTSHVKPDPPHIKRLFFQNGNLYVQWKNPQNFYSRCLSYQV
                                                                                                                                                              KCTWLPGRNTSPDTNYTLYYWHSSLGKILQCEDIYREGQHIGCSFALTNLKDSSFEQHSV
                                                                                                                                                                                                                         HRSKEVPLNERICLOVGSOCSTNESDNPSILVEKCTPPPEGDPESAVTELOCVWHNLSYM
                                                                                                                                                                                                                                                                                  GGVAAPTETOPPVTNLSVSVENLCTVIWTWNPPEGASPNCTLRYFSHFDNKQDKKIAPET
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80.9%;

24;

Score 1878; DB 4; Pred. No. 2e-176; Pred. No. 36; Indels

Length 405;

Gaps

141

60

120

300

240

180

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PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                    APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                                                                                                                                                   50, Application 5. 6703360
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FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,94
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEO ID NOS: 32
SOFTWARE: FRSTSEQ for Windows Version 3.
SEQ ID NO 32
LENGTH: 793
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US-10-282-162-32
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US-09-313-942-32
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US-09-313-942-32
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Best Local S
Matches 341
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                                                   APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/2
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US-09-313-942-30
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FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,94
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR PRIOR DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-25
NUMBER OF SEQ ID NOS: 32
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NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows
SEQ ID NO 32
LENGTH: 793
                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 30
LENGTH: 784
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/09313942 Patent No. 6472179
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Best Local Similarity
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
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Pred. No. 2.9e.
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58, Appl 30, Appl 30, Appl 30, Appl 30, Appl 30, Appl 30, Appl 82, Appl 82, Appl 82, Appl 82, Appl 84, Appl 16, Appl 16, Appl 17, Appl 16, Appl 17, Appl 16, Appl 17, Appl 16, Appl 17, Appl 17, Appl 18, Appl 19, Appl 10, Appl 11, Appl 11,

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Total number of hits satisfying chosen parameters:
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1072.443 Million cell updates/sec
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                              US-11-182-384A-4
US-11-149-309-37
US-11-149-309-37
US-10-850-270-4
US-11-036-568-4
US-11-155-843-125
US-09-828-9958-50
US-09-935-868-34
US-09-935-868-32
US-09-935-868-42
US-09-935-868-38
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US-11-067-251-3
US-11-185-230-4
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Biocceleration
Sequence 9, Appli
Sequence 4, Appli
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Sequence 37, Appli
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Sequence 125, Appli
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Sequence 32, Appli
Sequence 33, Appli
Sequence 44, Appli
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                                                                                                                                                                                                             LENGTH: 427 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-671-697-9
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US-10-671-697-9
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/671,697
FILING DATE: 29-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/545,002
FILING DATE: 06-APPR-2000
APPLICATION NUMBER: US 08/969,125
FILING DATE: 12-NOV-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10671697 Publication No. US20040043921A1 GENERAL INFORMATION:
                                                                                                                                    Query Match
Best Local Simi
Matches 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
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GAUCHAY, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                      Similarity 99.8 26; Conservative
                                                                    99.5%; Score 2309.5; DB 4; Length 427;
Similarity 99.8%; Pred. No. 2.9e-188;
6; Conservative 0; Mismatches 0; Indels 1; Gaps
MEWPARLCGLWALLLCAGGGGGGG-APTTOPPVTNLSVSVENLCTVIWTWNPPEGASS
           NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP 119
                                 MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
1234 5674 9 จากปกเริ่นการสามาเรา 2687
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US-10-850-270-10
US-09-313-942-30
US-09-935-868-30
US-10-287-1035-30
US-11-134-114-30
US-10-872-061A-82
US-09-825-561A-82
US-09-935-868-44
US-09-935-868-44
US-11-067-251-10
US-11-067-251-12
US-11-067-251-14
US-11-067-251-14
US-11-067-251-14
US-11-067-251-14
US-11-067-251-16
US-09-935-868-40
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Regult No.

Length

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Pred. No. is th score greater t and is derived

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60

Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Sequence: Title: Perfect score:

US-09-051-843D-4 2320 1 MEWPARLCGLWALLL

Scoring table:

BLOSUM62

Gapop 10.0 ,

Gapext 0

OM protein - protein search, using sw model

Copyright

July

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

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RESULT 2
US-11-067-251-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 2020A
CURRENT APPLICATION NUMBER: US/11/067,251
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 60/548,541
PRIOR FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: 60/602,139
PRIOR FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: 60/602,343
PRIOR APPLICATION NUMBER: 60/628,343
PRIOR FILING DATE: 2004-11-16
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/11067251 Publication No. US20050191730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                          LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapien
-11-067-251-3
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APPLICANT: Fairhurst, Jeanette
TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
   181
                                   180
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                                                                                    PEGDPESAVIELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
                                                                                                                                 NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
                                                                                                                                                                                                     MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
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QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
                                                               PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
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Pred. No. 2.9e-188;
0; Mismatches 0;
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US-11-185-230-4
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APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Vita, Natalio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity FILE REFERENCE: IVD924 US CNT 1 CURRENT APPLICATION NUMBER: US/11/185,230 CURRENT FILING DATE: 2005-07-18 PRIOR APPLICATION NUMBER: PCT/FR96/01756 PRIOR APPLICATION NUMBER: PCT/FR96/01756 PRIOR FILING DATE: 1996-11-07 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT 3
ORGANISM: Homo sapiens
FEATURE:
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                                                                               GVLPDTLNTVRIRVKINKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
                 IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE
                                                                 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
                                                                                                                                 DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
                                                                                                                                                                                                     QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
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ilarity 99.8%;
Conservative
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Pred. No. 2.9e-188;
0; Mismatches 0;
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TITLE OF INVENTION: Purified polypeptides having IL-
FILE REFERENCE: IVD924 US DIV 2
CURRENT APPLICATION UNMBER: US/11/182,384A
CURRENT FILING DATE: 2005-07-15
PRIOR FILING DATE: 1998-09-177,817
PRIOR FILING DATE: 1998-09-177,817
PRIOR FILING DATE: 1998-09-17-6
PRIOR FILING DATE: 1996-017-6
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEYSION 3.3
SEQ ID NO 4
RESULT 5
US-11-183-599A-4
; Sequence 4, Application US/11183599A
; Publication No. US20060035856A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
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; TYPE: PRT
; ORGANISM: HOMO s
US-11-182-384A-4
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US-11-182-384A-4
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APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pass
APPLICANT: Laurent, Pat
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Laurent, Patrick
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Pred. No. 2.9e
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Sequence 37, Application US/11149309
Publication No. US20060063228A1
GENERAL INFORMATION:
APPLICANT: Kasaian, Marion T.
APPLICANT: Tchistiakova, Lioudmila
APPLICANT: Weldman, Geertruida M.
APPLICANT: Marquette, Kimberly Ann
APPLICANT: Tan, Xiang-Yang
APPLICANT: Donaldson, Debra D.
APPLICANT: Donaldson, Debra D.
APPLICANT: Lin, Laura Long
APPLICANT: Shane, Tania
APPLICANT: Tam, Amy Szepui

APPLICANT:

Shane, Tania
Tam, Amy Szepui
Feyfant, Eric
Wood, Nancy L.
Fitz, Lori J.

APPLICANT

RESULT 6 US-11-149-309-37

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-599A-4
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Best Local Similarity
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PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
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Laurent, Patrick
Vita, Natalio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2309.5; DB 6;
Pred. No. 2.9e-188;
0; Mismatches 0;
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RESULT 7
US-10-850-270-4
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           Sequence 4, Application US/10850270
Publication No. US20050058645A1

GENERAL INFORMATION:

APPLICANT: AMRAD Operations Pty Ltd (for all States except the APPLICANT: Dunlop, Felicity (US only)

APPLICANT: Dunlop, Felicity (US only)

APPLICANT: Baca, Manuel(US only)

APPLICANT: Nash, Andrew (US only)

APPLICANT: Fabri, Louis (US only)

APPLICANT: Fabri, Louis (US only)

ITILE REFERENCE: 12175890/EJH

CURRENT APPLICATION NUMBER: US/10/850,270

CURRENT FILING DATE: 2004-05-20

COURTENT FILING DATE: 2004-05-20
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Best Local S
Matches 426
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 37
LENGTH: 427
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TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor FILE REBERENCE: 16158-048001 / AM101493

CURRENT APPLICATION NUMBER: US/11/149,309

CURRENT FILING DATE: 2005-06-09

PRIOR APPLICATION NUMBER: US 60/578,473

PRIOR FILING DATE: 2004-06-09

PRIOR APPLICATION NUMBER: US 60/581,375

PRIOR APPLICATION NUMBER: US 60/578,736

PRIOR FILING DATE: 2004-06-02

PRIOR FILING DATE: 2004-06-09

PRIOR FILING DATE: 2004-06-09
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APPLICATION NUMBER:
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Parris, Kevin D.
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Pred. No. 2.9e-188;
0; Mismatches 0;
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US-10-036-568-4
                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-036-568-4
                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10036568 Publication No. US20020090682A1 GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 427
                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                    APPLICANT: Willson, Tracy
APPLICANT: Nicola, Nicos A.
APPLICANT: Hilton, Douglas J.
APPLICANT: Metcalf, Donald
APPLICANT: Zhang, Jian G.
TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
TITLE OF INVENTION: ENCODING SAME
FILE REFERENCE: Davies CC
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Best Local Similarity
                                                                                                        CURRENT APPLICATION NUMBER: US/10/036,568
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US/09/051,843
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 11
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PRIOR APPLICATION NUMBER: AU 2003900437
PRIOR FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 28
                 ORGANISM: Human
                                   TYPE: PRT
                                                      LENGTH: 426
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               IL-13 receptor alpha-chain
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Pred. No. 1.2e-187;
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APPLICANT: Knopf, John
APPLICANT: Widom, Angela M.
APPLICANT: Widom, Angela M.
TITLE OF INVENTION: IL-13 BINDING AGENTS
FILE REFERENCE: 16158-020001
CURRENT APPLICATION NUMBER: US/11/155,843
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 60/581,078
PRIOR FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 11/149,025
PRIOR APPLICATION NUMBER: US 11/149,025
PRIOR FILING DATE: 2005-06-09
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 125
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US-11-155-843-125
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                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-843-125
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GENERAL INFORMATION:
APPLICANT: TChistiakova, Lioudmila
APPLICANT: Kasaian, Marion T.
APPLICANT:
                         Query Match
Best Local Similarity
Matches 424; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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Best Local
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Gill, Davinder
Jin, Macy X.
Jacobson, Bruce
Goldman, Samuel J.
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                         Score 2296.5; DB 6;
Pred. No. 3.8e-187;
0; Mismatches 2;
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US-09-828-995B-50
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; ORGANISM: Canis familiaris US-09-828-995B-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 405
TYPE: PRT
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APPLICANT: McCall, Catherine A.
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
COUNTAINED DESCRIPTION OF SEQ ID NOS: 104
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202 QIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEV 261
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FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/10/753,159
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 50
LENGTH: 405
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Best Local Similarity
Matches 345; Conserv
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APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13
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; Pred. No. 1.9e-151;
24; Mismatches 36;
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                                                                                                                   APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-935-868-34
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Patent No. US20020164690A1
GENERAL INFORMATION:
                                                                                    SEQ ID NO 32
LENGTH: 793
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TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
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TYPE: PRT
ORGANISM: Homo Sapiens
                                                 TYPE: PRT
ORGANISM: Homo
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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US-11-220-888-1
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US-11-297-957-4
US-11-301-764-3
US-11-301-764-71
US-10-511-937-2426
US-11-301-764-114
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US-10-953-349-18546
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US-11-331-993-7
US-11-331-993-7
; Sequence 7, Application US/11331993
; Publication No. US20060110800A1
; Publicati INFORMATION:
GENERAL INFORMATION:
Jame
Query Match
                                                                                                                                                                                                                  TELEFAX: 206-442-6678 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/11/331,993
FILING DATE: 04-Jun-1998
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/090,867
FILING DATE: 04-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E.
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-33
TELECOMMUNICATION: INFORMATION:
                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIF: 9810;
COMPUTER READDABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics,
STREET: 1201 Eastlake Ave
CITY: Seattle
STATE: WA
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Foster, Donald C.
Grant, Frank J.
O'Hara, Patrick J.
OF INVENTION: Testis-Specific Receptor
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US-11-155-109-10
US-11-259-133-2
US-11-293-697-2595
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US-10-511-937-2988
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US-10-449-902-43013
US-10-953-349-18547
US-11-259-133-6
US-10-953-349-32271
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  Score 302;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2005-09-07
PRIOR APPLICATION NUMBER: PCT/US2004/009354
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US 60/457,898
PRIOR FILING DATE: 2003-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 238603
CURRENT APPLICATION NUMBER: US/11/220,888
CURRENT FILING DATE: 2005-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GATELY, Stephen C.
APPLICANT: WANASKI, Stephen P.
TITLE OF INVENTION: IL 13 RECEPTOR ALPHA 2 ANTIBODY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE OTHER INFORMATION: Interleukin 13 receptor, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 380
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      224
                                      213 KPSFNIVPLTSRVKPDPPHIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQT
                                                                                 166
                                                                                                                    154
                                                                                                                                                         108 LLPWQC-TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLL 165
                                                                                                                                                                                           100 ----QCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ---- OCSTNESEKPSILVEKC--ISPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 RSSYFTFQLQNIVKPLPPVC--LTCTQESLYEIKLKWSIPLGPIPARCFVYEIEIREDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 KPSFNIVPLTSRVKPDPPHIKNLSFHNDDLY---VQWENPQNFI-SRCLFYEVEVNNSQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                  DTNYTLYYWHRSLEKIHOC-ENIFREGOYFGCSFDLTKVKDSSFEOHSVQIMVKDNAGKI
                                                                                                                                                                                                                                    WOPPLSLDHFKECTVEY----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHT 107
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RSSYFTFQLQNIVKPLPP--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT
                                                                             DTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPI
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                                                                                                                                                                                                                                                                                                                Score 294.5; DB 7;
Pred. No. 1.4e-17;
9; Mismatches 138;
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US-11-331-993-2
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farrah, Theresa M.
Foster, Donald C.
Grant, Frank J.
O'Hara, Patrick J.
TITLE OF INVENTION: Testis-Specific Receptor
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/090,867 FILING DATE: 04-Jun-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/331,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baumgartner, James
                                  100 ----QCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSP
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108 LLPWQC-TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLL 165
                                                                     53 WOPPLSLDHFKECTVEY----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHT
                                                                                                          51 WNPPEGAS--SNCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS
                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parker, Gary E.
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-Jun-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: WA
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27.0%;
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                                                                                                                                            Score 294.5; DB 7
Pred. No. 1.4e-17;
9; Mismatches 138
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Result
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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geneseqp2005s:*
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geneseqp2002s:*
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geneseqp2003bs:*
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                      AEE93788

AEF57817

ADF17835

ADL71814

AAE13745

ADF2207

ADF92207

ABW02180

AAF92208

ABW02181

AAF92208

ABW02181

AAF92208
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ADX97531
AAW24973
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ADL71812
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ADN62575
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AEC31473
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Aaw09822 Human int
Adx97531 Pandereati
Aaw24973 Human int
Aab19807 Human int
Adb19807 Human int
Adl182843 Human pRO
Adn04504 Antipsori
Adn62575 Human int
Abm82441 Tumour-as
Aec31473 Human IL-
Ae699788 Human int
Aef57817 Anti-IL-I
Adf17813 Human int
Aef17814 Human int
Aae13744 Human int
Aae13745 Human int
Aae13745 Human int
Aae13746 Human IL-
Abw02180 IL-13/IL-
Abw02180 IL-13/IL-
Abw02181 Human IL-
Add17813 Human IL-
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allergy; asthma; therapy.

NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine;

Human interleukin-12 receptor alpha chain NR4

15-JUL-1997 AAW09822;

(first entry)

AAW09822 standard; protein;

426

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ALIGNMENTS

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RESULT 1
AAWO9822
ID AAWO
XX
AAWO9822
ID AAWO
XX
AC AAWO
XX
CONT 15-J
XX
NR4;
KW NR4;
KW alle
XX
HOMO
XX
HOM
XX
H
23-OCT-1995;
22-DEC-1995;
                                                                                           23-OCT-1996;
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95AU-00006135
95AU-00007276
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/note= "Ig-like domain"
36
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/label= Cytoplasmic_tail
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RESULT 2
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AC ADX9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822), designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain. The human NR4 amino acid sequence was deduced from a composite DNA sequence (AAT66165) derived from bone marrow cDNA clones. Recombinant NR4, or fusion proteins including NR4, can be produced in transformed host cells. The receptor molecules and their components are useful in the development of a range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor, esp. for the development of cpds. capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of allergy,
   21-APR-2005
                                ADX97531;
                                                            ADX97531 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding animal haemopoietin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma and other conditions relating to IgE
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                                                                                                                                                                                                                                      VLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIEN
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(first entry)
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Best Local S
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Lichtner R,
                                                                                                                                                                                                                                                                                                                                        organic molecule, particularly having a molecular weight below 5000, especially 300, that binds to the pancreatic DNA, an aptamer or (monoclonal) antibody, preferably human or humanized, that binds to the pancreatic DNA, or an anti-idiotypic antibody raised against the monoclonal antibody, any of which may be derivatized with a reporter group, cytotoxic compound, immunostimulant and/or radioisotope. The nove human pancreatic proteins and their encoding DNA have cytostatic activity. The novel sequences are useful for inhibiting transcription and/or expression of genes and proteins associated with pancreatic cancer. This sequence represents one of the novel human pancreatic proteins of the invention. Note: This sequence is not shown in the specification, it has been electronically downloaded from a DVD-rom provided with this specification by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreas and its encoded protein. The invention further comprises: proteins and peptides, preferably isolated, that contain a sequence encoded by the novel nucleic acid, and methods for diagnosis and treatment of pancreatic cancer, using a substance that inhibits or binds to the protein or its DNA, including: an antisense oligonucleotide, short interfering RNA or ribozyme directed against the pancreatic protein, an interfering RNA or ribozyme directed against the pancreatic protein, and interfering RNA or ribozyme directed against the pancreatic protein.
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                                                                                                                                                                                                                                                                                                            Sequence 414
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(SPEC/)
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DB; ADX97460.
                                                                146 LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                                                                                                                                                                         401;
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SPECHT T.
                                                                                                                                                                                                                                                            Similarity
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KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
                                   LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                                     EVPLNERICLOVGSOCSTNESEKPSILVEKCISPPEGDPESAVTELOCIWHNLSYMKCSW
                                                                                                                                 EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                                                                                                                                        APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI
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Staub E,
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel human nucleic acid sequence of th protein. The invention further comprises:
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Pred. No.
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RESULT 3
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AX Huma
XX Inte
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                                         This sequence represents interleukin-13 (IL-13) alpha receptor. The cinvention relates to new purified peptides comprising 380 or 427 amino acid sequences, which are receptors for interleukin-13 (IL-13); the 380 cm 427 aa proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13R beta and alpha respectively. The IL-13R beta has high affinity when associated with the IL-4 receptor. Nucleic acids encoding IL-13R beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and callergy. Il-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard inmunoassays) to diagnose disease associated with abnormal expression of Overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified human interleukin-13 receptors - and related nucleic useful for diagnosis and treatment of inflammation, allergy, etc.
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Query Match Best Local Similarity

94.1%; 100.0%;

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atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                          Key
                     13-DEC-1996;
                                          12-NOV-1997;
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(GAUC/) GAUCHAT J.
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                                                                                                                                                                        receptor superfamily"
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                                                                                                                                                                                                                          /label=_Extracellular_domain
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                 label= Transmembrane_domain
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Best Local Simi
Matches 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a protein capable of binding human interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated from a human activated tonsilar cDNA library. This IL-13 receptor alpha-1 polypeptide can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells, useful in the treatment of diseases in which IgE or Th2
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                                                                                              ADL71812 standard;
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interleukin-13 receptor alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRR8I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 1A;
                                                                                                                                                                                                                                                                                                                SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                      LPGRNTSPDTNYTLYYWHRSLEKIHQCENI FREGQYFGCSFDLTKVKDSSFEQHSVQIMV
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                                                                                                                                                                      EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ
                                                                                                                                                                                        EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ
                                                                                                                                                                                                                                                                                                SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKINKLCYEDDKL
                                                                                                                                                                                                                                                                                                                                                          KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
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100.0%;
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Pred. No.
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Best Local S
Matches 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ] eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, ast or AIDS, comprises administering a polypeptide or soluble polypeptide.
                                                                                                                                                                                                                                                              gene therapy. The prese (IL-13 Ralpha) protein.
                                                                                                                                                                                                                                       Sequence 427
                                                                                                                                                                                                                                                                                                                                                                                           Claim
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12-NOV-1997;
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GAUCHAT J
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                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL71811
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KDNAGKIKPSENIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
                                  LPGRNTSPDTNYTLYYMHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                               LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                     EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                                                                  EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                                                                                                       APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKODKKIAPETRRSI
                                                                                                                                                    APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI
                                                                                                                                                                                       Conservative
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97US-00969125
2000US-00545002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.
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                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                   Score 401;
Pred. No.
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RESULT 6
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                                        antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, transiently, rheumatoid architis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis or anaemia for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and graveniar of theraparitically useful in twan are useful in the development
                                                                                                                                                                                                                                                                                                                                                                  New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmung mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human.
                                                                                                                                                                                                                                                            The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
                                                                                                                                                                                                                                                                           The present invention relates to PRO proteins and their coding so
The PRO proteins are useful for diagnosing and treating a B cell
                                                                                                                                                                                                                                                                                                                                        Claim
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                                 screening
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)B; ADL82842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark H,
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Query Match

94 1.18;

Score 401;

В 8,

Length 427;

The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.

Sequence

427

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RESULT 7
ADN04504
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                                                                                     WPI; 200
N-PSDB;
                                                                                                                                   Bodary
Wu TD;
                                          New PRO nucleic acid or polypeptide, useful for preparing pharmaceutical composition for diagnosing or treating pso
 Claim 9;
                                                                                                                                                                                                        25-SEP-2002; 2002US-0414006P
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                                                                                                                                                                                                                                                                     08-APR-2004.
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                                                                                                                                                                                                                                                                                                                            Homo sapiens
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DB; ADN04503.
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                                                                                                                                               Clark H,
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ID NO 898; 3069pp; English.
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                                                                                                                                                                                                                                                                                                                                                       therapy; psoriasis; diagnosis.
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Matches 401;
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                                                                                                                                                                                                                                            inflammatory bowel disease; multiple sclerosis; Alzheimer's disease; Lupus erythematosus; thyroiditis; diabetes; uveitis; psoriasis; uriticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis; Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy; Lyme disease; tuberculosis; malaria; leichmaniasis.
                                                                                                                                                                                                                                                                                                             Human; receptor; cytokine; interleukin 13 receptor alpha 1 IL-4; atopy; atopic dermatitis; allergy; rhinitis; eczema; cancer; inflammatory disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN62575 standard;
                        13-DEC-1996;
12-NOV-1997;
                                                              06-APR-2000;
                                                                                                                  US6743604-B1
                                                                                                                                                        Protein
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(SMIK ) SMITHKLINE
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                        96GB-00025899.
97US-00969125.
                                                                                                                                                       /note= "Signal
27. .427
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                         /note= "Mature protein claimed in claim
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                                                                                                                                                                                                                                                                                                                          chain; IL-13; asthma; AIDS;
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WPI; 2004-409324/38.

N-PSDB; ADN02574.

New isolated nucleic acid molecule encoding a polypeptide capable of binding human IL-13 and/or binding human IL-4, useful in medicine, in diagnostics or for producing antibodies.

Claim 1; SEQ ID NO 9; 24pp; English.

The invention relates to an isolated nucleic acid molecule (ADN62574), which encodes the mature form of a polypeptide capable of binding human IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are vector comprising the nucleic acid molecule and a host cell comprising the vector. The nucleic acids are useful as probes or primers or in the analysis of allelic variation. The polypeptides are useful for binding human IL-13 and/or binding human IL-4 and act as inhibitors by interfering with the interaction between human IL-13 or IL-4 and their natural receptors. They can also be used in medicine, e.g. for treatment of diseases such as atopy, atopic dermatitis, allergy, rihinitis, eczema, asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and inflammatory bowel disease), multiple sclerosis, Alzheimer's disease, crohn's disease, byogran's syndrome, glomerulonephritis, ulcerative colitis, crohn's disease, buberculosis, malaria and leichmaniasis. They can also be used for producing antibodies, which can be used for diagnosing diseases. The present sequence represents IL-13 receptor alpha 1 subunit.
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Matches Best Local Query Match 327 326 207 147 146 401; 87 98 27 26 Similarity EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ WSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFK SQTETHNVFYVQBAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV EVPLNERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW EVPLNERICLOVGSOCSTNESEKPSILVEKCISPPEGDPESAVTELOCIWHNLSYMKCSW APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI WSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFK SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ Conservative 94.1%; Score 401; 100.0%; Pred. No. 0, Mismatches 0; DΒ 8; 0 Length 427 Indels 0; Gaps 385 145 326 266 265 206 205 146 98 386 0

RESULT 9
ABM82441
ID ABM8
XX
AC ABM8
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ABM82441

protein;

ABM82441;

18-NOV-2004

(first

entry)

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human tumour-associated antigenic target (T polypeptides, and their related nucleic acids. The TAT polypeptides overexpressed in cancer tissues compared normal tissues, and may serve as effective targets for the diagnosis and treatment of cancer mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; SEQ
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)B; ACN41073.
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RESULT 10
AEC31473
                                                                                                      27-FEB-2004;
17-AUG-2004;
16-NOV-2004;
WPI;
                                                                                                                                                                                                                                                            US2005191730-A1
                                                                                                                                                                                                                                                                                                                                      Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-13 receptor; fusion protein; therapeutic; antiasthmatic; antiallergic; dermatological; antiinflammatory; immunosuppressive; cytostatic; hepatotropic; anti-HIV; virucide; gastrointestinal-gen; antibacterial; fungicide; antiparasitic; antiulcer; antithyroid;
                                  Karow
                                                                                                                                                                                  25-FEB-2005; 2005US-00067251
                                                                                                                                                                                                                         01-SEP-2005
                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                     REGENERON
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                                  Fairhurst
                                                                                                      ; 2004US-0548541P.
; 2004US-0602139P.
; 2004US-0628343P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor alpha-1 SEQ ID
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                                                                       PHARM INC
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New nucleic acid molecules encoding polypeptides capable of binding interleukin-4 and interleukin-13, useful for diagnosing and/or treating asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer

Claim 1; ID NO 3; 35pp; English.

The invention relates to a novel nucleic acid molecule encoding a polypeptide. The fusion polypeptide consists (R1)x-(R2)y-F, where F 231 and 24-231 of a fully defined sequence of 231 amino acids (AEC31472), which sequences may comprise 1-10 modifications, R2 is fully defined sequence of 427 or 380 bp (AEC31473+AEC31474), which sequences may comprise one to three modifications, F is a fusion component, and x and y are each independently a positive integer 1. 1 is a multimerizing component, a serum protein, or a molecule capable where the multimerizing component fusion R1 is 1 Ø The e of

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin-derived domain, a cleavable region (C-region), an amino acid sequence between 1-500 amino acids in length, optionally comprising at least one cysteine residue, a leucine zipper, a helix loop motif, or a coil-coil motif. The immunoglobulin-derived domain is the Fc domain of 19G or the heavy chain of 19G. A fusion protein of the invention has antiasthmatic, antiallergic, heavy collision is the feather than the following the invention as antiasthmatic, antiallergic, heavy chain of the heavy chain of the invention has antiasthmatic, antiallergic, heavy chain of the invention has immunosuppressive. Cytostatic heavy chain of the invention has immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                            Humani nterleukin-13
                                    pulmonary fibrosis; allergious
inflammatory bowel disease;
                                                                                                                                                                                                                                             protein co-ordinate data; protein structure; crystallography;
Antiasthmatic; Antiallergic; Cytostatic; Respiratory-Gen.;
                                                                                                                                                                                                                                                                                                        Monoclonal antibody; IL-13 alpha receptor; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                         Immunosuppressive; Dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     alpha
                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                    Crohns disease; cirrhosis; scleroderma
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Pred. No.
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SWISSPROT; 2006-067089/07. SPROT; P78552.

that

with

crystalline composition/complexes that comprises an antibody (where the antibody comprises an anti-IL-13 antibody or a Fab fragment of an anti-IL-13 antibody in complex with IL-13 or IL-13 alpha receptor), use of a three-dimensional model of an antibody to design an agent that interacts with an IL-13, a software system/computer for storing/analyzing information relating to a structure of an IL-13 polypeptide bound to an antibody, modulating IL-13 activity in a subject, treating a subject having a condition associated with IL-13 activity, a method of prophylactically treating a subject susceptible to a condition associated with IL-13 activity, a method of The invention relates to a crystalline antibody (I), where the directory and anti-interleukin (IL)-13 antibody or its Fab fragment, and Ti-4R Claim Crystalline antibody useful for designing agent polypeptide, comprises anti-IL-13 antibody capat 13 polypeptide to which IL-4R polypeptide binds is capable of binding a site of an IL-13 polypeptide to which an IL-4F (interleukin-4 receptor) polypeptide binds in vivo. Also included are SEQ ID NO 12; 318pp; English capable binds in e of binding so vivo. site h IL-13 of IL-עם

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                                                                                                                                                                                                                                                                                                              antiasthmatic; dermatological; respiratory-gen.; immunosuppressive antiinflammatory; cytostatic; virucide; antiilalergic; gastrointestinal-gen.; vaccine; antibody; diagnosis; therapeutic; antiasthmatic; chronic obstructive pulmonary disease; respiratory-infection; virucide; autoimune disorder; infection; virucide; autoimune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the methods above in the manufacture of a medicament for the prophylaxis or treatment of a condition associated with II-13 activity. The antibody crystal and methods are useful for designing an agent that interacts with an II-13 polypeptide. The agent is useful for treating an II-13 condition chosen from allergic asthma or nonallergic asthma, cancer, airway inflammation, eosinophilia, fibrosis, excess mucus production, inflammatory condition of the skin, gastrointestinal organs, blood vessels or connective tissue, and an autoimmune condition of the skin, gastrointestinal organs, blood vessels, or connective tissue, chronic obstructive pulmonary disorder, cystic fibrosis, pulmonary fibrosis, allergic rhinitis, atopic dermatitis, inflammatory bowel disease, Crohn's disease, Cirrhosis, scleroderma, or Hodgkin's lymphoma. The present sequence is the human IL-13 alpha receptor protein.
                                                                                                                                                                                                       immunosuppressive; immune disorder; inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.; gastrointestinal disea inflammation; allergic rhinitis; antiallergic; ear, nose, throa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody against human interleukin-13, useful for diagnosing, preventing, and/or treating a disorder, e.g. asthma, tumors, allergic rhinitis, or inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Widom AM,
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EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ
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                                                      WSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFK
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Parris KD,
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2004US-0578736F
2004US-0581375F
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100.0%; Pred. No.
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RESULT 13
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Best Local Similarity
Matches 331; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel antibodies that function as interleukin 13 receptor alpha-1 chain (II-13R alpha-1) antagonists and can be used for treating certain conditions induced by II-13. Specifically, it refers to antibodies that bind to II-13R alpha-1 and inhibit or modulate II-13 and II-4 induced signalling. II-13 is a mediator in the immunostimulatory system, such that it is involved in the induction of IgE, IgG4 and Thelper cells and accordingly is implicated in conditions from anaphylaxis to hay fever and asthma. As such, the present invention describes these novel antibodies as antiinflammatory, cytostatic, antiulcer, dermatological, antiallergic and antiasthmatic. The methods and compositions are useful for treating various disorders including fibrosis, hodgkin's disease, ulcerative colitis, scleroderma, allergic relations and chronic obstructive pulmonary in the procession of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2002; 2002AU-00001301.
03-FEB-2003; 2003AU-00900437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IL-13 alpha 1 receptor (IL-13R) protein.
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                                 EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
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                                                                                                                                                                                                       APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRR8I
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EVPLNERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
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interleukin (II)-13 and/or II-4 in the presence of II-4 Ralpha. The invention also relates to a method of treatment of a disease in which II-13 and II-4 cause adverse effects. The method is useful for treating a disease in which II-13 and II-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides of the invention are useful in raising antibodies. It is also useful in gene therapy. The present sequence is human interleukin-13 receptor alpha (II-13 Ralpha) mutant protein. Note: This sequence is not shown in the specification, however it is constructed based on human II-13 Ralpha protein shown as SEQ ID NO:9 in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asti or AIDS, comprises administering a polypeptide or soluble polypeptide.
                                                                                                                                                                                                                                                                                          The invention relates to polypeptides capable of binding human interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha
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12-NOV-1997;
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                                                          Novel soluble receptor polypeptides and polynucleotides used as cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoietic cells and for suppressing immune response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myasthenia gravis; systemic lupus erythematosus; SLE; di
ulcerative colitis; inflammatory bowel disease; Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disorder; haemostatic; cell proliferation; immune disord autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; mvasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthm
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28-JUL-2000; 2000US-0222121P
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DB; AAD22979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zalphall; cytokine receptor; immunosuppressive; cytostatic;
                                                                                                                                                                                                                                                                                         ZYMOGENETICS
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                      Page 236-237;
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                    243pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention relates to an isolated soluble zalphall cytokine receptor CC polypeptide and their cDNA molecules. Zalpha proteins are useful for CC inhibiting or antagonising the ligand activity-induced proliferation of CC haematopoletic cells and haematopoletic cell progenitors preferably CC Zalpha is useful for treating immune and inflammatory disorders, for CC zalpha is useful for treating immune and inflammatory disorders, for CC zalpha is useful for treating immune and inflammatory disorders, for CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is CC useful for treating diseases that require immune regulation including CC useful for treating diseases that require immune regulation including CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, CC sepsis, viral infection (dengue virus infection) and cancer. The present Sequence is human soluble cytokine IL-13 receptor alphal (IL-13RA1) correction related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Database :
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PIR 80:*
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Gapop 60.0 , Gapext 60.0
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426
1 MEWPARLCGLWALLLCAGGG.....QTKEETDSVVLIENLKKASQ 426
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	э I	27.7	253	238	221	212	212	211	206	201	199	151	115	102	1621	1433	888	864	479	465	405	331	292	285	272	248	201	201	426	Length	•
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איזים דירוו מיסרפ		htmorphetical proto	+	pro		spore germination	ted to prolin) prepr		20.2	hypothetical prote	bone morphogenetic	60S acidic ribosom	ic	-tyrosine	bullous pemphigoid	tyrosine kinase -	ine	cript	man	etical	e iymp	۳.	e memb				ernative aplic	IL-13Ralpha 1 prot	Description	

ОУ	Query Ma Best Loc Matches	RESULT 2 C40040 alternative splicing C;Species: Homo sapic C;Date: 24-Jan-1992; C;Accession: C40040 R;Ge, H; Zuo, P; M; Cell 66; 373-382, 199 A;Title: Primary str. A;Reference number: J A;Accession: C40040 A;Status: preliminary A;Molecule type: mRNJ A;Roesidues: 1-201 <gr a;cross-references:="" domain:="" f;122-182="" f;17-81="" i="" ribor="" ribor<="" td=""><td>Query Best I Match Match Qy</td><td>RESULT 1 JC7773 IL-13Ralph C;Species: C;Date: 01 C;Accession R;Pierrot, Biochem. B; A;Title: E; A;Title: E; A;Reference A;Accession A;Molecule A;Rocession A;Molecule C;Comment: C;Genetics A;Gene: i1.</td><td></td><td></td></gr>	Query Best I Match Match Qy	RESULT 1 JC7773 IL-13Ralph C;Species: C;Date: 01 C;Accession R;Pierrot, Biochem. B; A;Title: E; A;Title: E; A;Reference A;Accession A;Molecule A;Rocession A;Molecule C;Comment: C;Genetics A;Gene: i1.		
18 99	atc Sal	native stative	Matc local es 36	RESULT 1 JC7773 JC7773 JC7773 JC7777 C;Species: Rattus norv C;Date: 01-Feb-2002 #s C;Accession: JC7773 R;Pierrot, C.; Benique Biochem. Biophys. Res. A;Title: Expression of A;Reference number: JC A;Accession: JC7773 A;Molecule type: mRNA A;Residues: 1-426 <pie a;cross-references:="" a;gene:="" c;comment:="" c;genetics:="" i1-37alpha1<="" proteil="" td="" this="" un=""><td></td><td>U & U N P O O O O O O O A O N P O</td></pie>		U & U N P O O O O O O O A O N P O
	simil	splicing iomo sapi como sapi an-1992 C40040 0.382, 19 mary str number:	ωω	ha 1 protein Rattus norv Rattus norv 1-Feb-2002 #s on: JC7773 on: JC7773 Expression of ce number: JC on: JC7773 e type: mRNA s: 1-426 <pie eferences:="" proteis="" proteis<="" s:="" td="" this="" un=""><td></td><td><i>Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა</i></td></pie>		<i>Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა</i>
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27 108	2.3 100. tive	or ASF man) ence_r , J.L. e of ti 0; MUI: 0; MUI: leoprote	10.13 ity 100.0 servative IIIFPPIPDPO	cat cus lence L.; E nmmun. funct funct 73; PN		257 257 256 256 256 256 257 257 357 357 357
	% ··	Frevi revi the JID:9	ĞKI ĞKI	rev rev lior 28 IID:		222211211112122
	o;	isi isi hu hu 913 rej in j	FKE O;	(Norway ra _revision Begue, A.; 1. 287, 965 tional IL- MID:115739		B84 T13 S00 T113 A34 A34 CCIP CCIP TVZ TVZ T127
	Score 10; DB 2; Length 20 Pred. No. 0.045; , Mismatches 0; Indels	uman 124-Jan-1992 #text, n 24-Jan-1992 #text, an splicing factor / 9149; PMID:1855257 9149; PMID:000017A38: eat homology <rrm1> epeat homology <rrm1></rrm1></rrm1>	10.1%; Score 43; DB 2; Length 42 imilarity 100.0%; Pred. No. 2e-35; Conservative 0; Mismatches 0; Indels YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 407	rat) on 01-Feb-2002 #text_ A.; Khalife, J. 969-976, 2001 IL-13Ralphal by rat B 73960 UNIPARC:UPI000017CC49 onally binding protei	ALIGNMENTS	B84346 T13591 S00276 TLBPM1 A34466 CIPGL CIRBL CTPGP CITUL S09860 TYZMMB S31415 B31219 T27609 T27609 T127609
	201; ls	nge reve	426; ls 07	change 09-Jul-2004 cells. ; GB:AY044251 n involved in B ce		hypothetical prote tail fiber adhesin tail fiber protein call fiber protein calpain (EC 3.4.22 hypothetical prote anthocyanin biosyn glycine-rich prote collagen 2 - Caeno hypothetical prote probable homeotic hypothetical prote
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A;Reference number: A40041; MUID:91309150; PMID:1830244 A;Accession: B40041 A;Status: preliminance
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nucleic acid binding protein - rice
;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
C;Accession: T02745; T02718
R;Yoon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.
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T02745
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Cell 6, 373-382, 1991
A;Title: Primary structure of the human splicing factor
A;Title: number: A40040; MUID:91309149; PMID:1855257
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C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992
C;Accession: A40040; B40041
C;Accession: A40040; B40041
R;Ge, H.; Zuo, P.; Manley, J.L.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
F;17-81/Domain: ribonucleoprotein repeat homology <RRM1>
F;122-182/Domain: ribonucleoprotein repeat homology <RRM2>
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A; Residues: 1-248 < KR
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R;Krainer, A.R.; Mayeda, A.; Kozak,
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Pred. No.
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Pred. No.
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R;Ge, H.; Zuo, F.; Famer, Cell 66, 373-382, 1991
Cell 66, 373-382, 1991
A;Title: Primary structure of the human splicing factor ASF
A:Deference number: A40040; MUID:91309149; PMID:1855257
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B40040
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S69312
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C;Keywords: transmembrane protein
F;142-158/Domain: transmembrane ##
F;201-217/Domain: transmembrane ##
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1998
A;Description: The rice genome contains at least two different genes
A;Reference number: Z14712
A;Accession: T02745
                                                                                                C;Species: Homo sapiens (man)
C;Date: 24-Jan-1992 #sequence_revision
C;Accession: B40040
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A; Map position: 12R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, January 1994 A;Description: The sequence of S. cerevisiae cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane protein YLR338w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8300.13-a
C;Species: Saccharomyces cerevisiae
C;Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 09-J
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A;Experimental source: strain Ilpoombyeo
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A; Residues: 1-181, 183-272 < YO2>
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A; Residues: 1-272 < YOO>
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A; Residues: 1-285 < DUZ>
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                                                                                                                                                             alternative splicing factor ASF-2 -
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                                                                                                                    24-Jan-1992 #text_change
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                                            reveals similarities with
                                                                                                                          31-Dec-2004
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sus scrofa
mus musculu
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oryza sativ
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oryza sativ
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P78522; 095646; 099556;
01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
01-NMY-1997, sequence version 1.
07-MAR-2006, entry version 50.
Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).
Name-IL13RA1; Synonyms=IL13R, IL13RA;
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                           Ferrara P.; "Cloning of the human IL-13R alphal chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex."; FEBS Lett. 401:163-166(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=T-cell;
MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;
Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;
"CDNA cloning and characterization of the human interleukin 13
receptor alpha chain.";
J. Biol. Chem. 271:29265-29270(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                             TISSUE=Carcinoma; MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7; MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ.
                                                                                                                                                                                                                                                                                                                                                                  Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
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Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage P. Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                           Q5r7h2
Q3yla6
Q3uch2
Q7kr12
Q6dii2
Q6dii2
Q49216
Q49221
Q6h7a7
Q7sxp4
Q07955
Q6pdm2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wada M., Hisano T., Kuwano M.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
        SFRS1_HUMAN
SFRS1_MOUSE
SFRS1_MOUSE
Q3YLAG_PIG
Q3YCH2_MOUSE
C7KR12_DROME
SFRS1_CHICK
SFRS1_CHICK
SFRS1_CHICK
G1921_CNYSA
Q49226_ORYSA
Q49221_ORYSA
Q7921_ORYSA
Q795Q1_NSYSA
Q795Q1_NSYSA
                                                                                                                                                     ALIGNMENTS
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SF1L1
SFRS1
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NCBI_TaxID=9606;
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Q6z541
Q59fa2
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Q5jkr1
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Q6avt7
       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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113R1_MOUSE
Q8C1Z3_MOUSE
Q561K3_RAT
Q8VHC2_RAT
Q8VHC2_RAT
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Q5JSL4 HUMAN
Q59EG2 HUMAN
Q9UDY5 HUMAN
Q7YRV5 MACFA
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2: uniprot_trembl:*
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Match Length
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                      TIGSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver, skeletal muscle and ovary; lowest levels in brain, lung and kidney. Also found in B-cells, T-cells and endothelial cells. DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Sohnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                              and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling, but cannot replace the function of gamma c in allowing enhanced IL2 binding activity.

-!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1, and possibly other components.
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R EMBL; Y09328; CAA70508.1; -; mRNA.

R EMBL; U62889; AAB37127.1; -; mRNA.

R EMBL; BC009960; AAH09960.1; -; mRNA.

R EMBL; BC009960; AAH09960.1; -; mRNA.

R H-INUDB; HIX0017089; -.

R H-GNC; 5974; IL13RA1.

R MIM; 300119; gene.

R GO; GO:0005898; C:interleukin-13 receptor complex; TAS.

R GO; GO:0005898; C:interleukin-13 receptor complex; TAS.

R GO; GO:0005898; C:interleukin-13 receptor inked signal transdu...;

R InterPro; IPR002996; Cytkn_rcpt_B/G.

R InterPro; IPR003996; Cytkn_rcpt_B/G.

R InterPro; IPR003596; Cytkn_rcpt_B/G.

R GO; GO:000506; Hempt_rcpt_S/F2.

R GIycoprotein; Membrane; Receptor; Signal; Transmembrane.
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/FTId=PRO_0000010939.
Extracellular (Potential).
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TISSUB-Colon;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RITAUSDERG R.L., Feligoold E.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Worley A.A., Young A.C., Shevchenko Y., Shevchenko Y., Shevchenko Y.,

Raha S.S., Worley A., Young A.C., Shevchenko Y., Soulfard G.G.,

Raha S.M. Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roherztion and initial analysis of more than 15,000 full-length human
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                             94.1%; Score 401; DB 1; Length 427; 100.0%; Pred. No. 0; O; Mismatches 0; Indels
  130 T -> I (in Ref. 3).
358 G -> D (in Ref. 3).
48760 MW; 5983B3E8F554107B CRC64;
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01-DEC-2001, sequence version 1.
FFBB-2006, entry version 23.
Interleukin 13 receptor, alpha 1,.
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130 1.
358 3.
427 AA;
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NUCLEOTIDE SEQUENCE.
                                                                                                      Similarity
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Q96BB4; Q8WX08;
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  CONFLICT
CONFLICT
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                    NUCLEOTIDE SEQUENCE
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                                NCBI_TaxID=9606;
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                                                                                          for proper protessport and cell-
                                               Ensembl; ENSG0000131724; Homo sapiens.

60, G0:0016621; C:integral to membrane; IEA.

G0; G0:004896; F:nembrane; IEA.

G0; G0:004896; F:nembrane activity; IEA.

InterPro; IPR002996; Cyth. rcpt S.P.

InterPro; IPR003332; Hempt rcpt S.P.

InterPro; IPR003332; Hempt rcpt S.P.

INTERPRO; IPR003345; HEMPT CPC S.P.

INTERPRO; IPR003362; HEMATOPO_REC_S.P.; I.
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                                                                                                                                                                                                                                                                                                            DB 2; Length 427;
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                                                                                                                                                                                                                                                                                     48677 MW; E6A42F7466A39A09 CRC64;
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           'roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                          94.1%; Score 401;
                                                                                                                                                                                 EMBL; BC015768; AAH15768.1; -; mRNA.
                                                                                                                               activation (By similarity).
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Best Local Similarity 100.0
Matches 401; Conservative
mouse cDNA sequences.
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                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                      427 AA;
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Q5JSL4;
                                         TISSUE=Colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .; IEA
                                                                                                                                                                               Lawlor S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Membrane; single-pass type I membrane
protein (By similarity).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
-!- DOMAIN: The box I motif is required for JAK interaction and/or
Chordata, Craniata, Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini; Hominidae;
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Ensembl; RNGG0000131724; Homo sapiens.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain.)
GO; GO:0004895; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn ropt B/G.
InterPro; IPR003532; Hempt_ropt SF2.
PROSITE; PS013156; HEMPTOPO_REC_S_F2; 1.
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100.0%; Pred. No. v,
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  activation (By similarity).
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les 401; Conservative
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NCBI_TaxID=9541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVPLNERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 EVPLNERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELOCILHNLSYMKC6W 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
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                                                                                                                                                                                                                                                                                                                                EMBL; AB209849; BAD93086.1; -; mRNA.
Ensembl; ENSG0000131724; Homo sapiens.
G0; G0:0016220; C:membrane; IEA.
G0; G0:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
G0; G0:0004872; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn rept B/G.
InterPro; IPR003532; Hempt rept S/F.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=IL13RA1; ORFNames=RP13-12804.2-002;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Chordata, Craniata, Vertebrata, Buteleostomi;
Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 APTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
                                                                                                                                                            s,
                                                                                                                                    TISSUE-Aorta endothelial cell;
Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                          Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 AA; 48555 MW; 342A3A6F7347261B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMFGDONDDTLHWKKYDIYEKQTKEETDSVVLIENLKKASQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 300; DB 2; I 99.8%; Pred. No. 2.3e-291; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000, integrated into UniProtKB/TrEMBL 01-MAY-2000, sequence version 1. 21-FEB-2006, entry version 26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 99.8'
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                               NUCLEOTIDE SEQUENCE.
                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UDY5 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
NON TER
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HUMAN
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145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                      -!- SUBCELLUILAR LOCATION: Membrane; single-pass type I membrane protein (By similarity).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding (By similarity).
-!- DOMAIN: The box I motif is required for JAK interaction and/or activation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 EVPLNERICLÓVGSÓCSTNESEKPSILVEKCISPPEGDPESAVTELÓCIWHNISYMKCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGOYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKODKKIAPETRRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVPLINERICLOVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKODKKIAPETRRSI
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Bukaryota, Metacoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016021; C:initegral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoletin/interferon-class (D200-domain.
GO; GO:0004872; F:receptor activity; IEA.
Interbro; IPR002999; Cytkn.ropt B/G.
Interbro; IPR003532; Hempt_ropt_S F2.
PROSITE; PG01366; HEMATOPO_REC_S_F2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                         Wada M., Hisano T., Kuwano M.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              Lawlor S.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 58.9%; Score 251; DB 2; Le
Local Similarity 100.0%; Pred. No. 2.1e-242;
les 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U81380; AAD00511.2; -; mRNA.
EMBL; AL391280; CAI41409.1; -; Genomic_DNA.
Ensembl; ENSG0000131724; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003, sequence version 1.
07-FEB-2006, entry version 12.
Interleukin 13 receptor alpha 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Transmembrane
                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=IL13Ral;
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NUCLEOTIDE SEQUENCE.
                Query Match
Best Local Similarity
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QGUGT1_
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                        326 LYITMLLIVPVIVAGAIIVLLIYKKKKKKIKIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYD 385
                                                                                                                                                                                                                                                                                                                                                                                                             343 LYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYD 402
                                                                                                                  EMBL, AY312267; AAP78901.1; -; mRNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004895; F:hemacopoietin/interferon-class (D200-domain. .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002996; Cytkn rept B/G.

InterPro; IPR003532; Hempt_rept B/G.

PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashira H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
21-FEB-2006, entry version 7.
CDNA FLJ41521 fis, clone BRTHA2012980, moderately similar to
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (IL-13R-ALPHA-1) (IL- 13RA- 1).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                      interleukin 13 receptor alpha 1.
                                                                                                                                                                                                                                                                                             33.8%; Score 144; DB 2; Length 409; 100.0%; Pred. No. 5.4e-135; tive 0; Mismatches 0; Indels
                          Maccarone P., Drinkwater C.C., Nash A.D.; "Cynomolgus monkey interleukin 13 receptor alpha 1."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  409 AA; 46685 MW; 9B98A52671686AF4 CRC64;
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GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 IYEKQTKEETDSVVLIENLKKASQ 426
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                                                                                                                                                                                                                                                                                                                          Conservative
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              NUCLEOTIDE SEQUENCE.
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SEQUENCE
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226 AA; 24825 MW; 0CBE8208934F18DF CRC64;

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                                                                                                                                                                                                                             336 GKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDT 395
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GO; GO:0016020; C:membrane; I:mRNA.
GO; GO:0016020; C:membrane; I:membrane; I:membrane; I:membrane; I:membrane; I:membrane; I:membrane; I:membrane; I:merpro; I:membrane; I:m
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                      136 GKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDFGKIFKEMFGDQNDDT
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                                                                                                                                             Gaps
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086326
01-JUN-2003, integrated into UniProtKB/TrEMBL.
01-JUN-2003, sequence version 1.
21-FEB-2006, entry version 14.
Interleukin 13 receptor alpha 1.
Sus scrofa (Pig).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazes; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
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                                                   Length 226;
Score 91; DB 2; Length 420-
Pred. No. 4.20-82;
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100.0%; Pred. No. 8.3e-56;
tive 0; Mismatches 0;
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                       21.4%; bcc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           396 LHWKKYDIYEKQTKEETDSVVLIENLKKASQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 LHWKKYDIYEKQTKEETDSVVLIENLKKASQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 AA.
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                                                                                                                                        91; Conservative
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0863Z6 PI
1D 08633
AC 0863
DT 01-J
DT 21-C
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43;
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MEDLINE=22380257; PubMed=12477932; DOI=10.073/pnas.242603899;

MEDLINE=22380257; PubMed=12477932; DOI=10.073/pnas.242603899;

MA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worlby K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AIIVLLLYLKRLKIIFPPPPPPPRFKEMFGDQNDDTLHWKKYDIYEKQTKEFTDSVVL 414
                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002996; Cythn rcpt B/G.

InterPro; IPR003532; Hempt_rcpt S_F2.

PROSITE; PS01356; HEWATOPO_REC_S_F2; 1.
                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                         Pubmed-15350752; DOI=10.1016/j.vetimm.2004.05.003;

Zarlenga D.S., Dawson H., Kringel H., Solano-Aguilar G.,

Zarlenga D.S., Dawson H., Kringel H., Solano-Aguilar G.,

"Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor

1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and

Trichuris suis infections on tissue mRNA levels.";

Vet. Immunol. Immunopathol. 101:23-234 (2004).

-!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane

protein (By similarity).

-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                423 AA; 47985 MW; EA636FE6BCA533D9 CRC64;
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                                                                                                                                                                                                                surface receptor binding (By similarity).
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Matches 62; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                          EMBL; AY266142; AAP23301.1; -; mRNA.
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O7-FBB-2006, entry version 18.
1113ral protein (Fragment).
Name=1113ral;
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                               NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9823;
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Q8VDP7;
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113R1 MOUSE
D 113R1 MOUSE STANDARD; PRT; 424 AA.
AC 019R1 MOUSE STANDARD; PRT; 424 AA.
D 019R1 MOUSE STANDARD; PRT; 424 AA.
AC 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1997, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE INTER-2006, entry version 2.
DE INTER-10 (Interleukin-13-binding protein) (NR4) (CD213a1 antigen).
CM Name=Ill3ra1; Synonyms=Ill3ra; Ill3ra;
CM Name=Ill3ra1; Synonyms=Ill3ra; Oraniara: Ruteleostomi;
CM Name=Ill3ra1; CANDARD (MOUSE).

MUS musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=96133964; PubMed=8522669; DOI=10.1073/pnas.93.1.497;
Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
Willson T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AA; 29044 MW; E303CF276C7A6E81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 2; Le
Pred. No. 6.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005615; C:extracellular space; RCA. GO; GO:0016021; C:integral to membrane; RCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSMUSG0000017057; Mus musculus.
MGI; MGI:105052; Ill3ral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC021472; AAH21472.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%;
                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
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01-WAR-2003, integrated into UniProtKB/TrEMBL.
01-WAR-2003, sequence version 1.
21-FEB-2006, entry version 22.
Colon RCB-0549 Cle-H3 cDMD, RIKEN full-length enriched library, clone:G430044106 product:interleukin 13 receptor, alpha 1, full insert
                                                                                   Name=Ill3ral;
                                                                                                                                                                                          rissum=colon;
                                                                                                                                                                                                                                                                                   rissum=Colon;
                                                                                                                                                                                                                                                                     NUCLEOTIDE
                                                                        sednence
        DDTTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDD
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Marra M.A.;
Tand mouse cDNA sequences.", 99:16899-16903 (2002).
Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Can form a functional receptor for IL13. Also serves as an alternate accessory protein to the common cytokine receptor gamma chain for IL4 signaling, but cannot replace the function of gamma chain for IL4 signaling, but cannot replace the function of gamma claim allowing enhanced IL2 binding activity (By similarity).
Cir SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
Cir SUBCELULAR LOCATION: Membrane; single-pass type I membrane
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                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                       testis, stomach, brain, skin, and colon; but not skeletal muscle.
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-
                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-13 receptor alpha-1 chain.
                                                                                                                                                                                                              protein.
-!- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
                                                                                                                                                                                                                                                                             surface receptor binding. DOMAIN: The box 1 motif is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S80963; AAB50695.1; -; mRNA.
EMBL; BC052425; AAH52425.2; -; mRNA.
EMBL; BC052939; AAH59939.1, -; mRNA.
EMS.; BC052939; AAH59939.1, -; mRNA.
EMS.; AAH59939; AAH59939.1, -; mRNA.
EMS.; CO00000107057; Mus musculus.
MGI; MGI:105052; 1113ral.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003596; Cytlm rcpt B/G.
InterPro; IPR003596; Cytlm rcpt B/G.
InterPro; IPR003532; Hempt_rcpt S/F2;
PROSITE; PS01356; HEMATOPO_REC_S F2; 1.
Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
SIGNAL
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9.8e-34;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EB8330A0DC82C9F9 CRC64;
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N-linked (GlCNAc...)
N-linked (GlCNAc...)
N-linked (GlCNAc...)
N-linked (GlCNAc...)
N-linked (GlCNAc...)
Potential.
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100.0%; Pred. No. >...
... 0; Mismatches
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Best Local Similarity 100.0
Matches 43; Conservative
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59
103
136
262
338
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171
424 AA;
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262
338
                                                                                                                                                                                                                                                                                                        activation.
                                                                                                                                                                                                                                                                                                                                    subfamily
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DISULFID
SEQUENCE
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TRANSMEM
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424 AA

PRT;

PRELIMINARY;

Q8C1Z3 MOUSE Q8C1Z3;

Q8C1Z3 MOUSE ID Q8C1Z3 MC AC Q8C1Z3;

RESULT 12

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RA Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic VUB., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic VUB., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic VUB., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic VUB., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Rabasia M., Barsal M., Bersano T., Bono H., Chalk A.M., Ranaluk D., Down T., Engstrom P., Fagiolini M., Faulkner G., R. Fetcher C.F., Fukushima T., Furuno M., Rutaki S., Gariboldi M., Ratcher C.F., Fukushima T., Furuno M., Rutaki S., Gariboldi M., Ratcher C.F., Fukushima T., Furuno M., Rutaki S., Gariboldi M., Ratcher C.F., Fukushima T., Engstrom P., Fagiolini M., Faulkner G., Alt M., Kanapin A., Katch M., Kawaswa Y., Kelso J., Kitamura H., R. Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., R. Kitamo H., Kollias G., Krishman S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., R. Kurochkin I.V., Lareau L.F., Madan Babu M., Madcar M., Marchionni L., R. Matsuda H., Matsuzawa S., Mki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Mottagui-Tabar S., Reed J., Reid J.F., Ring B.Z., Ringwal K., Saltaka S., Nori F., Ohara O., Rochaber C., Sekigura K., Saltaka S., Nori F., Ohara O., R. Schonbach C., Sekigurchi K., Sandelin A., Scholder C., Sekigura K., Sultan B., Sheng Y., A Schonbach C., Sekigura K., Sultan B., Sheng Y., R. Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Ramanoja K., Tan S.L., Liu E.T., Rawajishi H., Zabarovsky E., Zhu C., Sanaki D., Tapana Y., Hammond S.M., Taeadala R.D., Liu E.T., Brusic V., Quackehbush J., Ramanci K., Itah M., Nakao J., Hammond S.M., Taeadala R.D., Liu E.T., Brusic V., Quackehbush J., Ramanci H., Rawashima M., Rato T., Kawajishi H., Rawashima T., Kodima M., Kato T., Kawajishi T., Kodima M., Nakao J., Saltaki M., Saltaki M., Saltaki M., Saltaki M., Saltaki M., Salta
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Colon;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Nazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schrimi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothi C., Corbani L.E., Cousins S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Anai A., Kawaji H., Kawaswa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin IV., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Ravasi T., Reed J.C., Reed D.J., Reid B.Z., Ringwald M.,
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Schneider C., Semple C.A., Sectou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Werardo R., Wagner L., Wahlestedt C., Wang Y., Ward M., Saha K.,
Wanna Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hinozane-Kishikawa T., Konno H., Nakamura M., Saha Z.,
RA Miyazaki A., Sakai K., Kawai J., Aizawa K., Shinagawa A.,
Rahiraki T., Waki K., Kawai J., Shibata K., Shinagawa R.,
Rahiraki T., Waki K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Soshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA Farmahysis of the monuse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rochiman W., Casaterland T., Gissi C., King B., Kochiwa H., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Barke J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Rarchionni L., Mashima J., Mazzarelli J., Mondoerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Nasabii S., Kawaishi S., Kaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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TISSUE=Colon;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausbergg R.L., Feingold E.A., Grouse L.H., Derge J.G., Stausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 184 multicapillary sequencer."; genome Res. 10:1757-1771(2000).
                                                                                       Bono H., Car.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AA; 48371 MW; 4B45EB0B76EEB83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 9.8e-34; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AK089984; BAC41028.1; -; mRNA.
Ensembl; RNSMUSGO000017057; Mus musculus.
MGI; MGI:105052; Illaral.
GO; GO:0005615; C:extracellular space; RCA.
GO; GO:0016021; C:integral to membrane; RCA.
InterPro; IPR002995; Cyth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Conservative
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                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                    TISSUE=Colon;
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10-MA
AC Q561K
AC Q561K
DT 10-MA
DT 21-FE
DE INTER
GGN Name
OC Bukar
OC Bukar
OC Mamma
OC NACBI
RN [1]
RP TISSU
RR TISSU
RR ACT
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Sequence 4215, A Sequence 4360, A Sequence 43619, A Sequence 34401, A Sequence 49137, A Sequence 42121, A Sequence 52121, A Sequence 52121, A Sequence 54211, A Sequence 42341, A Sequence 54590, A Sequence 38261, A

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Sequence 727, Application US/11134871
Fublication No. US20060141528A1
GENERAL INFORMATION:
APPLICANT: Abebreadid, Rudolf H.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Quantification of Serum Glycoproteins FILE REFERENCE: 6661-116
CURRENT APPLICATION NUMBER: US/11/134,871
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: 60/573,593
FRIOR PILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 3602
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3230, Application US/11134871

Publication No. US20060141528A1

GENERALI INCORMATION:
APPLICANT: Arbersold, Rudolf H.
APPLICANT: Zhang, Hui
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Quatification of Serum Glycoproteins
FILE REFERENCE: 66661-116
CURRENT APPLICATION NUMBER: US/11/134,871
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: 60/573,593
PRIOR APPLICATION NUMBER: 60/573,593
NUMBER OF SEQ ID NOS: 3602
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 17; DB 7; Length 17; 100.0%; Pred. No. 7.5e-10; tive 0; Mismatches 0; Indels
US-10-449-902-42360
US-10-449-902-43679
US-10-449-902-43679
US-10-449-902-43179
US-10-449-902-49137
US-10-449-902-49137
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  LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 17; Conserv
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US-11-134-871-3230
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Sequence 33310, Ap
Sequence 33266, A
Sequence 51366, A
Sequence 51866, A
Sequence 51821, A
Sequence 5621, A
Sequence 2683, Ap
Sequence 2683, Ap
Sequence 9576, Ap
Sequence 3746, Ap
                                                                                        July 8, 2006, 01:31:52 ; Search time 21 Seconds (without alignments) 544.307 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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426
1 MEWPARLCGLWALLLCAGGG......QTKEETDSVVLIENLKKASQ
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             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-134-871-3230

US-10-449-902-32626

US-10-449-902-32626

US-10-449-902-51966

US-10-449-902-51966

US-10-449-902-56221

US-10-611-814-18

US-10-953-349-14842

US-10-953-349-9576

US-10-953-349-9574

US-10-953-349-9576

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US-10-953-349-9576

US-10-953-349-9576

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US-10-953-349-9576

US-10-449-902-28815

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                                                                  - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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6238
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Sequence 51966, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT PAPLICATION NUMBER: US/10/449,902

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOUTHARD: PARCHING UNCY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FLING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR FLING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR SEQ ID NOS: 56791
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2.3%; Score 10; DB 6; Length 176; 100.0%; Pred. No. 0.034; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      ; Sequence 43265, Application US/10449902
; Publication No. US20060123505A1
     Query Match 2.3
Best Local Similarity 100.
Matches 10; Conservative
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US-10-449-902-51966
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US-10-449-902-43265
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US-10-449-902-51966
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LENGTH: 285
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Sequence 33914, Application US/10449902

Publication No. US20060123505Al

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-39

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 175

TENGTH: 175

TENGTH: 175
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Sequence 32626 Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-20369

PRIOR APPLICATION NUMBER: UP 2002-383870

PRIOR APPLICATION NUMBER: UP 2002-383870

PRIOR PLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SEQ ID NO 32626

LENGTH: 176
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                                                                                                                                         2.3%; Score 10; DB 7; Length 25; 100.0%; Pred. No. 0.0063; ative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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  LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Oryza sativa
US-10-449-902-33914
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US-10-449-902-32626
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Perfect score:
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   US-09-688-286D-4
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US-09-913-942-32
US-09-949-016-8550
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Sequence 32, Appl
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RESULT 2 US-08-969-125-9

Sequence 9, Application Patent No. 6143871
GENERAL INFORMATION:

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TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125B
FILING DATE: 12-No. 6143871-1997
                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: NIXON &
STREET: 1100 NORTH
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TITLE OF INVENTION: SUBSTANCES AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BONNEFOY,
                                                                                                                                                                                 Similarity 100.
01; Conservative
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LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
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                                       EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                              EVPLNERI CLQVGSQCSTNESEKPSI LVEKCI SPPEGDPESAVTELQCIWHNLSYMKCSW
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TOPOLOGY: linear
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                                                                       Best Local Sir
Matches 401;
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/969,125
FILING DATE: 12-No. 6743504-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
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TITLE OF INVENTION: SUBSTANCES AND THEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BONNEFOY, JEAN-YVES
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NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955
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STATE: VIRGINIA
COUNTRY: U.S.A.
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                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                           TELEPHONE: (70 TELEFAX: (703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-No. 6743604-1997
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                                                                       Score 401; DB; Pred. No. 0; Mismatches
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6094
LENGTH: 427
TYPE: PRT
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Best Local S
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Patent No. 6814...
PATERAL INFORMATION:
VENTER,
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                                                                                                                                                                                                                                                                                     Matches
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-09-949-016-6094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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6812339
                                                                                                                      LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV 205
   SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
                                                                KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN 265
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                                                                                                        LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
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                                               KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
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US-09-313-942-30

Sequence 30, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS,
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APPLICANT:
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; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-82
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Best Local Similarity
Matches 317; Conserv
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APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sprecher,
APPLICANT: No. 6777;
APPLICANT: West, Jan
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5. 6777539
WSNWSQEMSIGKKRNST
                                                                    SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
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                                               SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
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West, James W.
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100.0%; Pred. No. 5.4e-310;
tive 0; Mismatches 0;
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418 205 358 145 298

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GENERAL INFORMATION:
GENERAL INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR APPLICATION NUMBER: DCT/US99/22045
PRIOR APPLICATION NUMBER: 09-09-22
PRIOR APPLICATION NUMBER: 09-09-22
PRIOR APPLICATION NUMBER: 09-09-22
PRIOR FILING DATE: 1999-09-22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 784
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CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 784
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US-10-282-162-30
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; ORGANISM: Homo sapiens
US-09-313-942-30
                                                                                        ; TYPE: PRT
; ORGANISM: Homo
US-10-282-162-30
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                 Query Match
Best Local Similarity
Matches 317; Conserv
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Best Local
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                     Conservative
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                                74.4%; Score 317; D
100.0%; Pred. No. 1.
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Pred. No. 1.3e-309;
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                                  .3e-309;
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITILE OF INVENTION: RECEPTOR BASED ANTAGONIS
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 199-05-19
PRIOR APPLICATION NUMBER: 09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR TILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
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US-09-313-942-32
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Best Local Similarity
Matches 317; Conserv
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Patent No. 6472179
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                                                             SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
                                                                                                            KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNN
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WSNWSQEMSIGKKRNST 342
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Sequence 8550, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
VUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 793
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Best Local :
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Patent No. 6927044
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APPLICANT: REGENERON PHARMACEUTICALS,
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100.0%; Pred. No. 1.3e-309;
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RESULT 12
US-09-828-995B-50
; Sequence 50, Application US/09828995B
; Patent No. 6703360
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                                                                                                                                                                                  Query Match
Best Local Similarity 100.
43; Conservative
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8550
LENGTH: 233
TYPE: PRT
ORGANISM: Human
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wilson, Tracey
APPLICANT: Nicola , Nicos
APPLICANT: Hiton, Douglas
APPLICANT: Metcalf, Donald
APPLICANT: Zhang , Jian
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding
FILE REFERENCE: 23199-215
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: AU PN6135
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: AU PN7276
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: AU PP2208
PRIOR APPLICATION NUMBER: AU PP2208
PRIOR FILING DATE: 1996-09-09
NUMBER OF CEC ID NOC. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/688,286D CURRENT FILING DATE: 2003-07-10
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus
                                                                                                                                                                                                                                                                                                                                           ENGTH: 424
                                                                                                                          363 YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 405
                                                                                                                                               365 YLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQ 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HNLSYMKCSWLPGRNTSEDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 KIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTL 306
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                                                                                                                                                                                                                                                                                                    musculus
                                                                                                                                                                                                  10.1%; Score 43; DB 2; Le
100.0%; Pred. No. 1.4e-34;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine

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US-09-028-937-25
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 104
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PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: AL-7
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                   TELEFAX: (415) 949-8711 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/195,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 FILE REFERENCE: AL-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                        LENGTH: 405
                                                                                                                                                                                             APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,999
FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                   REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olsson, Lennart APPLICANT: Naranda, Tatjana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                  ENGTH:
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amino acid
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                  22 amino acids
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PRIOR APPLICATION NUMBER: 60/231,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8825
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                                   US-09-949-016-6323
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-6323
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Best Local Similarity
Matches 22; Conserv
                                                                                                           SOFTWARE: Fas
SEQ ID NO 6323
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6323, Application US/09949016
Patent No. 6812339
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                    TYPE: PRT
ORGANISM: Human
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TYPE: PRT
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                                                                                         LENGTH: 331
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100.0%;
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1.1e-14;
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Length 331;
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Title:
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seq length: 2000000000
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Match
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Gapop 60.0 ,
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  Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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(without alignments)
1049.625 Million cell updates/sec
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  GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration
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US-10-671-697-9
US-11-185-230-4
US-11-185-230-4
US-11-183-59A-4
US-11-183-59A-4
US-11-183-59A-7
US-10-850-70-4
US-10-850-70-6
US-09-825-561A-82
US-10-872-087-82
US-10-850-270-10
US-09-935-868-34
US-09-935-868-34
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 EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
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Result No.

Minimum DB Maximum DB

Word size Searched:

Database :

145	YMKCSW	QCIWHNLS	EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW	SILVEKCISPP	NESEKP	SQCSI	ICLQVG	EVPLNER	86 I	₹
86	ETRRSI)KQDKKIAP	CSLWYFSHFGD	TWNPPEGASSNC	ILCTVIW	VSVEN	PUTNLS	PTE	27 A	ਰੱ
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			USBS.	S COIS	10671697 21A1 JEAN-YVES JEAN-FRANCOIS	S/106 3921 <i>t</i> Y, JE	lication US/ US200400439 MATION: F: BONNEFOY, GAUCHAT, INVENTION:	z Hoio	1 71-69 nce 9 catic ERAL APF	IESULT 1 IS-10-671 Sequenc Publica GENER
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RESULT 2
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; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
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Matches 401
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 3
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TYPE: PRT
ORGANISM: Homo sapien
0-11-067-251-3
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APPLICANT: Fairhurst, Jeanette
APPLICANT: Fairhurst, Jeanette
TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
FILE REFERENCE: 2020A
CURRENT APPLICATION NUMBER: US/11/067,251
CURRENT FILING DATE: 2005-2-25
PRIOR APPLICATION NUMBER: 60/548,541
PRIOR FILING DATE: 2004-02-27
PRIOR FILING DATE: 2004-08-17
PRIOR FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: 60/602,139
PRIOR APPLICATION NUMBER: 60/602,139
PRIOR FILING DATE: 2004-01-11-16
PRIOR FILING DATE: 2004-11-16
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; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo s
; FEATURE:
Sequence 4, Application US/11182384A
Publication No. US200660035855A1
GENERAL INFORMATION:
APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pascual
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APPLICANT: Ferrara, Pascual
APPLICANT: Ferrara, Pascual
APPLICANT: Laurent, Patrick
APPLICANT: Vita, Natalio
TITLE OF INVENTION: Purified Polypeptides Having
FILE REFERENCE: IVD924 US CNT 1
CURRENT APPLICATION NUMBER: US/11/185,230
CURRENT FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 427
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SEQ ID NO 4
LENGTH: 427
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APPLICANT: Laurent, Patrick
APPLICANT: Vita, Natalio
TITLE OF INVENTION: Purified polypeptides having
FILE REFERENCE: IVD924 US DIV 1
                                                         CURRENT APPLICATION NUMBER: US/11/183,599A CURRENT FILING DATE: 2005-07-15 PRIOR APPLICATION NUMBER: 09/077,817 PRIOR FILING DATE: 1998-09-14 PRIOR APPLICATION NUMBER: PCT/FR96/01756 PRIOR FILING DATE: 1996-11-07 NUMBER OF SEQ ID NOS: 15
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APPLICANT: Vita, Natalio
TITLE OF INVENTION: Purified polypeptides having
FILE REFERENCE: IVD924 US DIV 2
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                                                               SOFTWARE: PatentIn version SEQ ID NO 37
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                                                                                                                                          APPLICANT: Tam, Amy Szepui
APPLICANT: Feyfant, Eric
APPLICANT: Wood, Nancy L.
APPLICANT: Widom, Angela M.
APPLICANT: Widom, Angela M.
APPLICANT: Barris, Kevin D.
APPLICANT: Goldman, Samuel J.
APPLICANT: Goldman, Samuel J.
APPLICANT: Goldman, Samuel J.
APPLICANT: Horion Number: US/11/149,309
CURRENT APPLICATION NUMBER: US/11/149,309
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/578,473
PRIOR APPLICATION NUMBER: US 60/581,375
PRIOR PILING DATE: 2004-06-22
DRIOR FILING DATE: 2004-06-22
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APPLICANT:
APPLICANT:
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                                                                                                NUMBER OF SEQ ID NOS: 37
                                                                                                                PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2004-06-09
                                               LENGTH: 427
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APPLICANT: Baca, Manuel(US only)
APPLICANT: Mash, Andrew (US only)
APPLICANT: Mash, Andrew (US only)
APPLICANT: Fabri, Louis (US only)
TITLE OF INVENTION: NOVEL peptides
FILE REFERENCE: 12175890/EDH
CURRENT APPLICATION NUMBER: US/10/850,270
CURRENT APPLICATION NUMBER: US/10/850,270
PRIOR APPLICATION NUMBER: AU PS1301
PRIOR FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: AU 2003900437
PRIOR FILING DATE: 2003-02-03
PRIOR FILING DATE: 2003-02-03
NUMBER OF SEQ ID NOS: 28
SECTION RESEARCH STATES AND APPLICATION SET ON APPLICATION NUMBER: AU 2003900437
PRIOR FILING DATE: 2003-02-03
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LENGTH: 427
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: human
           146
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31; Conservative 0;
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LPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMV
                                                                                             EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
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                                                                                                                                                                                                                                                                                                          77.7%; Score 331; 100.0%; Pred. No.
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Pred. No. 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 322
TYPE: PRT
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Best Local Similarity
Matches 317; Conserv
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APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
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APPLICANT: No. US20020137677A1ak,
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
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100.0%; Pred. No. 3.5e-289;
tive 0; Mismatches 0;
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RESULT 9

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US-10-850-270-10

Sequence 10, Application US/10850270
Publication No. US20050058645A1
GENERAL INFORMATION:
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          APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
APPLICANT: Dunlop, Felicity (US only)
APPLICANT: Baca, Manuel (US only)
APPLICANT: Nash, Andrew (US only)
APPLICANT: Fabri, Louis (US only)
TITLE OF INVENTION: Novel peptides
FILE REFERENCE: 12175890/EJH
CURRENT APPLICATION NUMBER: US/10/850,270
CURRENT FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: AU 2003900437
PRIOR APPLICATION NUMBER: AU 2003900437
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Best Local Similarity 100.
Matches 317; Conservative
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SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 322
TYPE: PRT
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APPLICANT: Novak, Ju.
APPLICANT: West, Jamu
APPLICANT: Holly, Ric
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Publication No. US20040235743A1
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APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.

TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22D1

CURRENT APPLICATION NUMBER: US/10/872,087

CURRENT FILING DATE: 2004-06-18
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PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR ETLING DATE: 2001-04-03
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UMBER.
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AU 2003900437
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100.0%; Pred. No. 3.5e-289;
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APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 36
LENGTH: 776
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-935-868-36
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Best Local Sin
Matches 317;
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TYPE: PRT
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Conservative
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100.0%; Pred. No. 6.5e-289;
tive 0; Mismatches 0;
                                                                                                                                                                                                                 Score 317; DB 3; L; Pred. No. 7.5e-289; 0; Mismatches 0;
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RESULT 13

US-09-313-942-30

; Sequence 30, Application US/09313942

; Publication No. US20020012962A1

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN

; TITLE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942
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US-09-935-868-34
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LENGTH: 780
TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 317; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
NUMBER PatentIn version 3.0
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Pred. No. 7.5e-289;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/313,942
PRIOR TILING DATE: 1999-05-19
PRIOR PPLICATION UNMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-05-19
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US-09-935-868-30
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Best Local Similarity
Matches 317; Conserv
                                                                                                                                          Query Match
Best Local Similarity
Matches 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09935868
Patent No. US20020164690A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 30
LENGTH: 784
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
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TYPE: PRT
                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Homo sapiens
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EVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSW
                                                              APTETOPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSHFGDKQDKKIAPETRRSI
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                                                                                                                                                 74.4%; Score 317; DB 3; Liarity 100.0%; Pred. No. 7.5e-289; Conservative 0; Mismatches 0;
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Pred. No.
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Sequence 30, Application US/10287035

Publication No. US20030104567A1

GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
ITILE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
ITILE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
ITILE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 09/05-19
PRIOR APPLICATION NUMBER: 09/05-19
PRIOR APPLICATION NUMBER: 09/05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
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; ORGANISM: Homo sapiens
US-10-287-035-30
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                                                         SQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL 325
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WSNWSQEMSIGKKRNST 342
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Search completed: July 8, 2006, 01:34:51 Job time: 189 secs

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